

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: January 10, 2005, 17:38:42 ; Search time 166 Seconds

(without alignments)  
 2458.836 Million cell updates/sec

Title: US-10-053-758-225

Perfect score: 5961

Sequence: 1 MPAPRCAVRSLRSHRE.....TALEAANPALPSDFKTLID 1132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 160304 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	5961	100.0	1132	9 US-09-90-080-2	Sequence 2, Appli
2	5961	100.0	1132	9 US-09-749-728B-31	Sequence 2, Appli
3	5961	100.0	1132	9 US-09-843-676-225	Sequence 225, APP
4	5961	100.0	1132	9 US-09-933-052-2	Sequence 23, Appli
5	5961	100.0	1132	11 US-09-938-110A-23	Sequence 2, Appli
6	5961	100.0	1132	14 US-10-053-758-225	Sequence 225, App
7	5961	100.0	1132	14 US-10-208-243-2	Sequence 2, Appli
8	5961	100.0	1132	14 US-10-054-295-225	Sequence 225, App
9	5961	100.0	1132	14 US-10-054-611-225	Sequence 225, App
10	5961	100.0	1132	14 US-10-105-663-2	Sequence 2, Appli
11	5961	100.0	1132	14 US-10-044-692-2	Sequence 2, Appli
12	5961	100.0	1132	14 US-10-044-539-2	Sequence 2, Appli
13	5961	100.0	1132	14 US-10-295-681-57	Sequence 57, Appli

RESULT 1	US-09-90-080-2	Sequence 2, Application US-09990080
		Patent No. US-02012686A1
		GENERAL INFORMATION:
		APPLICANT: Morin, Gregg B.
		APPLICANT: Geron Corporation
		TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
		FILE REFERENCE: 018-258C
		CURRENT APPLICATION NUMBER: US-09-990, 080
		CURRENT FILING DATE: 1998-08-03
		PRIOR APPLICATION NUMBER: US 09-052, 864
		PRIOR FILING DATE: 1998-03-31
		NUMBER OF SEQ ID NOS: 21
		SOFTWARE: PatentIn Ver. 2.0
		SEQ ID NO: 2
		LENGTH: 1132
		TYPE: PRT
		ORGANISM: Homo sapiens
		US-09-90-080-2

ALIGNMENTS

Query	Match	100.0% ; Score 5961; DB 9 ; Length 1132;
Best Local Similarity	100.0% ; Pred. No. 0;	Mismatches 0 ; Indels 0 ; Gaps 0 ;
Matches 1132 ; Conservative 0 ;		
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Db	1 MPRAPCRAYRSLSLASHREVLPATEFVRRLGPQGWRLVORGDPAAFRALVAQCLVCVPW 60	
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Db	61 DARPPAAPSFRQVSCLKEVARYLQRCLERGAKNVLAFGPALUDGARGSPPEAFTSVR 120	
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 Db 181 ATQARPYPHASGPRLGCCRWNHSTREAGYPLGLPAPGARRRGSSASRSLPLPKPRRR 240  
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 Db 301 RQHHAGPSTSRRPRPDTCPCPVYAAETKHTLYSSGDEKEQLRSPFILLSPLTGARRL 360  
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 Db 421 PAAGVCAREKPGSVAPEEEEDTDPRRLVQLLRQHSSPWQYGFYRACIURLVPEGLGWS 480  
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 Db 481 RHNERFLRNTKFKISGKHAKLSQLELTNKMSVRDCAMURSPGYCUPAAEHLRZEEI 540  
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 Db 1081 KLTRHRVTVPLLGSLRATAOTOSRKLPGTTLTALEAANPALPSDFKTIID 1132  
 Qy ; APPLICANT: Fukuda, Keiichi  
 ; APPLICANT: Ogawa, Satoshi  
 ; APPLICANT: Sakurada, Kazuhiro  
 ; APPLICANT: Gojo, Satoshi  
 ; APPLICANT: Yamada, Yoji  
 ; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOM  
 ; FILE REFERENCE: 00716.000043  
 ; CURRENT APPLICATION NUMBER: US/09/7149,728B  
 ; CURRENT FILING DATE: 2001-09-17  
 ; PRIORITY APPLICATION NUMBER: H11-372826  
 ; PRIOR FILING DATE: 1999-12-28  
 ; PRIORITY NUMBER: PCT-JP00-01148  
 ; PRIOR FILING DATE: 2000-02-28  
 ; PRIORITY NUMBER: PCT-JP00-07741  
 ; PRIOR FILING DATE: 2000-11-02  
 ; NUMBER OF SEQ ID Nos: 80  
 ; SOFTWARE: PatentIn Ver.2.0  
 ; SEQ ID NO: 31  
 ; LENGTH: 1.132  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09/7149-728B-31  
 Query Match 100.0%; Score 5961; DB 9; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 2  
 US-09/7149-728B-31  
 ; Sequence 1, Application US/09749728B  
 ; Patent No. US2002014457A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Umezawa, Akihiro  
 ; APPLICANT: Hata, Jun-Ichi

Db 661 LFSVLYNERARRPGIIGASVGLDDIIRHAWRTFVLVRQAQDPPELYFVKVDTGAYDTI 720  
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RESULT 3  
 Sequence No.: US-09-843-676-225  
 Application US/098433676  
 Patent No.: US2002164786A1  
 GENERAL INFORMATION:  
 APPLICANT: Cech, Thomas R.  
 Lingner, Joachim  
 Nakamura, Toru  
 Chapman, Karen B.  
 Morin, Gregg B.  
 Harley, Calvin  
 Andrews, William H.  
 TITLE OF INVENTION: No. US20020164786A1e1 Telomerase  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, 8th Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States of America  
 ZIP: 94111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/854,050  
 FILING DATE: 26-APR-2001  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/854,050  
 FILING DATE: 09-MAY-1997  
 APPLICATION NUMBER: US/08/846,017  
 FILING DATE: 25-APR-1997  
 APPLICATION NUMBER: US/08/844,419  
 FILING DATE: 18-APR-1997  
 APPLICATION NUMBER: US/08/724,643  
 FILING DATE: 01-OCT-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Apple, Randolph T.  
 REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 225:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1132 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 225:  
 US-09-843-676-225  
 Query Match 100.0%; Score 5961; DB 9; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Missmatches 0; Indels 0; Gaps 0;  
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 781 QETSPRLDAVYIEQSSLNEASSGLFDVFLRFMCHAVRIRGKSYVOCOGIPQGSILSTL 840

**RESULT 4**  
**US-09-953-052-2**

Sequence - 2, Application US/0953052  
 Patent No. US2002017346A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
 Lingner, Joachim  
 Nakamura, Toru  
 Chapman, Karen B.  
 Morin, Gregg B.  
 Harley, Calvin B.  
 Andrews, William H.

TITLE OF INVENTION: Antisense Compositions for Detecting and Inhibiting Telomerase Reverse Transcriptase

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/953,052  
 FILING DATE: 14-Sep-2001  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/052,919  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: US 08/844,419  
 FILING DATE: 18-APR-1997  
 APPLICATION NUMBER: US 08/846,017  
 FILING DATE: 25-APR-1997  
 APPLICATION NUMBER: US 08/851,843  
 FILING DATE: 06-MAY-1997  
 APPLICATION NUMBER: US 08/854,050  
 FILING DATE: 09-MAY-1997  
 APPLICATION NUMBER: US 08/911,312  
 FILING DATE: 14-AUG-1997  
 APPLICATION NUMBER: US 08/912,951  
 FILING DATE: 14-AUG-1997  
 APPLICATION NUMBER: US 08/915,503  
 FILING DATE: 14-AUG-1997  
 APPLICATION NUMBER: US 08/914,549  
 FILING DATE: 19-NOV-1997  
 APPLICATION NUMBER: US 08/974,584  
 FILING DATE: 19-NOV-1997

US-09-953-052-2

Query Match 100.0%; Score 5961; DB 9; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MPAPRCAVRSLRSHYREVPLATVRLGPQWRLVQRGDPAAFLVAQCLVCVPW 60

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 Db 121 SYLPNTYDIALRGSGANGLLPPLRGGDDVYLHARCALEVLPAPSCAYQVCPPLYQLGA 180

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 Db 421 PAAGVCAREPKQGSVAPEEEDTPRLVQLRHQHSSPQVYGFVACRLRVPGWGWS 480

Qy 481 RHNERERFLRNTYKFIISLGKAHLSSLBLTWNMSVRDCAWLRSRPGYGCVPAAEHRLREEI 540  
 Db 481 RHNERERFLRNTYKFIISLGKAHLSSLBLTWNMSVRDCAWLRSRPGYGCVPAAEHRLREEI 540

Qy 541 LAKFLIWLMSYYVVELRSFFVTETTFOKRLFLFYRKSYNSKLSQSIGIROLHKLKVOLRE 600  
 Db 541 LAKFLIWLMSYYVVELRSFFVTETTFOKRLFLFYRKSYNSKLSQSIGIROLHKLKVOLRE 600

Qy 601 LSEAVYRQHREARPALTSRPFIPKPDGLRPIVNDYVVGARTPREKAERLTSRVKA 660  
 Db 601 LSEAVYRQHREARPALTSRPFIPKPDGLRPIVNDYVVGARTPREKAERLTSRVKA 660

Qy 661 LFSVNLAYERARPGLIGASVIGLDI1HRAWRTFVLRVRAODPBPFLFVVDVTGAYDTI 720  
 Db 661 LFSVNLAYERARPGLIGASVIGLDI1HRAWRTFVLRVRAODPBPFLFVVDVTGAYDTI 720

Qy 721 PQDRLETEVIASIIKPKONTYCVRVAVQXAVQXAHGHYRKAFKSHVSTLTDLQPYMRQQFVAHL 780



STATE: California  
 COUNTRY: United States of America  
 ZIP: 94111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0., Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/053,758  
 FILING DATE: 18-JAN-2002  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/854,050  
 FILING DATE: 09-MAY-1997  
 APPLICATION NUMBER: US 08/851,843  
 FILING DATE: 06-MAY-1997  
 APPLICATION NUMBER: US 08/846,017  
 FILING DATE: 25-APR-1997  
 APPLICATION NUMBER: US 08/844,419  
 FILING DATE: 18-APR-1997  
 APPLICATION NUMBER: US 08/724,643  
 FILING DATE: 01-OCT-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Apple, Randolph T.  
 REGISTRATION NUMBER: 36,129  
 REFERENCE/DOCKET NUMBER: 015389-00293 OUS  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 225:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1132 amino acids  
 TYPE: amino acid  
 TOPOLOGY: Linear  
 MOLECULE TYPE: protein  
 /SEQUENCE DESCRIPTION: SEQ ID NO: 225:  
 US-10-053-758-225

Query Match 100.0% Score 5961; DB 14; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Gaps 0;

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 Db 1 MPRAPPAFSRQVSCKELVARLQLRCERGAKNVLAFCFALLDARGGPPEAFTTSVR 120  
 Db 1 DARPPPAFSRQVSCKELVARLQLRCERGAKNVLAFCFALLDARGGPPEAFTTSVR 120

Query 1 MPRAPCRAYRSLLSHYREVPLATFVRRLGPQCWRLVQRGDDAAFRALVAQCLVCPW 60  
 Query 61 DARPPPAFSRQVSCKELVARLQLRCERGAKNVLAFCFALLDARGGPPEAFTTSVR 120  
 Query 61 DARPPPAFSRQVSCKELVARLQLRCERGAKNVLAFCFALLDARGGPPEAFTTSVR 120

Db 121 SYLPNTVTDAIRGSAGWGLIIRRVDVLLHLLARCALFVLVAPSCAVCGPPLYQGGA 180  
 Db 121 SYLPNTVTDAIRGSAGWGLIIRRVDVLLHLLARCALFVLVAPSCAVCGPPLYQGGA 180

Query 181 ATQARPPPHASGPRRLGCERAWNHSREAGVPLGLPAGARRGGASRSLPLPKRR 240  
 Query 181 ATQARPPPHASGPRRLGCERAWNHSREAGVPLGLPAGARRGGASRSLPLPKRR 240

Db 181 GAAPEPERTPVGQSWAHPRTRGSDRGFCVSPARAAEATSGLEGALSGRSHSPVG 300  
 Query 241 GAAPEPERTPVGQSWAHPRTRGSDRGFCVSPARAAEATSGLEGALSGRSHSPVG 300  
 Db 241 GAAPEPERTPVGQSWAHPRTRGSDRGFCVSPARAAEATSGLEGALSGRSHSPVG 300

Query 301 RQHHAGPSPSTSRPPWDTCPPVTAETKHFLYSGDQEQLRPEFLSSLRPSLTGARNL 360  
 Db 301 RQHHAGPSPSTSRPPWDTCPPVTAETKHFLYSGDQEQLRPEFLSSLRPSLTGARNL 360

Query 361 VETIPIGSRPWMPGCTPRLPRLPQRYWQMRPLPEFLLGNAQCPYGHILKTHCPLRAVT 420  
 Db 361 VETIPIGSRPWMPGCTPRLPRLPQRYWQMRPLPEFLLGNAQCPYGHILKTHCPLRAVT 420

Query 421 PAAGYCAREKPQGQSVAAPPEBDTDPRLVQLRHOSSPMQVXGVRACLRVLVPGMWS 480  
 Query 421 PAAGYCAREKPQGQSVAAPPEBDTDPRLVQLRHOSSPMQVXGVRACLRVLVPGMWS 480

Db 421 PAAGYCAREKPQGQAAPPEBDTDPRLVQLRHOSSPMQVXGVRACLRVLVPGMWS 480  
 Query 481 RHNNRERLNTKKEKISLGKAKLSLOELTWKMSYRDCAWLRRSPFGVGCUPAAFHLREBI 540  
 Query 481 RHNNRERLNTKKEKISLGKAKLSLOELTWKMSYRDCAWLRRSPFGVGCUPAAFHLREBI 540

Db 541 LAKELHWLMSSVYVLLSASSFFYVETTIFQKNRLFIFYKSWSKLSIGTROHJKRVLRE 600  
 Db 541 LAKELHWLMSSVYVLLSASSFFYVETTIFQKNRLFIFYKSWSKLSIGTROHJKRVLRE 600

Query 601 LSEAEVROREARPALTSRLRPTPKPDGLRPVNMDVVGARTFREKERAELTSRVKA 660  
 Query 601 LSEAEVROREARPALTSRLRPTPKPDGLRPVNMDVVGARTFREKERAELTSRVKA 660

Query 661 LFSUNYEFBARRPOLLGASVGLDIDHNPMPTEVLYRAQDPPELYPKVQDUTGAVDTI 720  
 Query 661 LFSUNYEFBARRPOLLGASVGLDIDHNPMPTEVLYRAQDPPELYPKVQDUTGAVDTI 720

Db 721 PQDLTEVITASIIKPKONTYCVRVAVIOKAANGHVKAPKSHVSLTDLQPYMRQFVYAHL 780  
 Db 721 PQDLTEVITASIIKPKONTYCVRVAVIOKAANGHVKAPKSHVSLTDLQPYMRQFVYAHL 780

Query 781 QETSPLRDAVIEQSSSLNEASSGLFDVFLRFNCMHAVIRGKSYVOCGIPQGSILSTL 840  
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Query 841 LCSCYGMENKLAFGTRDGLLRLVDELLJYTPHTHAKTEFLPTLVGVPDYSVCVNL 900  
 Query 841 LCSCYGMENKLAFGTRDGLLRLVDELLJYTPHTHAKTEFLPTLVGVPDYSVCVNL 900

Db 901 RKTVUNFPVEDEALGGTAFVQMPAHGLPPWCGLLDRTLVEQDSYYARYSTRASLTF 960  
 Db 901 RKTVUNFPVEDEALGGTAFVQMPAHGLPPWCGLLDRTLVEQDSYYARYSTRASLTF 960

Db 961 NRGFKAQNMRKLFGVLRKCHSLFLLDVOVSQTCTNIYKILLQAYRPHACVILQLP 1020  
 Db 961 NRGFKAQNMRKLFGVLRKCHSLFLLDVOVSQTCTNIYKILLQAYRPHACVILQLP 1020

Db 1021 PHQQWNKNPTFELRVISDTASLYCILKAKNAGMSLGAKGAGPLPSEAQMCHQAFLL 1080  
 Db 1021 PHQQWNKNPTFELRVISDTASLYCILKAKNAGMSLGAKGAGPLPSEAQMCHQAFLL 1080

Query 1081 KLTRHRTYVPLGSLRSTAQLSKLPGTTLTLEAAANPAPSDFTKTL 1132  
 Query 1081 KLTRHRTYVPLGSLRSTAQLSKLPGTTLTLEAAANPAPSDFTKTL 1132

RESULT 7  
 US-10-208-243-2  
 ; Sequence 2, Application US/10208243  
 ; Publication No. US2003004394A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Geron Corporation,  
 ; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune  
 ; Response to a Telomerase Antigen  
 ; FILE REFERENCE: 015389-003500PC  
 ; CURRENT APPLICATION NUMBER: US/10/208-243  
 ; CURRENT FILING DATE: 2002-07-30  
 ; PRIOR APPLICATION NUMBER: US/09/675,321  
 ; PRIOR FILING DATE: 2000-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/112,006  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIORITY APPLICATION NUMBER: WO PCT/US99/06898  
 ; PRIORITY FILING DATE: 1999-03-30  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 1132  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-208-243-2

Query Match	100.0% ; Score 5961; DB 14; Length 1132;	Db	1021 PHQQWKNPFPFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAQWLCHQAFLL 1080
Best Local Similarity	100.0% ; Pred. No. 0;		
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 MPRAPRCAVRSLLRSHYREVLPATFVRRLGPOGMRLVQRGDPAFAFRALVAQCLVCVPW 60	Qy	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
Db	1 MPRAPRCAVRSLLRSHYREVLPATFVRRLGPOGMRLVQRGDPAFAFRALVAQCLVCVPW 60	Db	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
Qy	61 DARPPPAAPSPQVSCKELVARVQLCERGAKVLAFLGPALLQARGPPEATTSVR 120		
Db	61 DARPPPAAPSPQVSCKELVARVQLCERGAKVLAFLGPALLQARGPPEATTSVR 120		
Qy	121 SYLPNTVTDALRGSGAWGLLRRGVDDVLVHLARCAFLVAPSCAYQVCGPPLYQLGA 180	Qy	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
Db	121 SYLPNTVTDALRGSGAWGLLRRGVDDVLVHLARCAFLVAPSCAYQVCGPPLYQLGA 180	Db	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
Qy	181 ATQARPPhASGPRRRLGICERAWNHSVREAGVPLGLPAPGARRGGSASSLPLPKRPRR 240		
Db	181 ATQARPPhASGPRRRLGICERAWNHSVREAGVPLGLPAPGARRGGSASSLPLPKRPRR 240		
Qy	241 GRAPEPTTPYQGQSMWAHPGTRGPSPDRGFCTVSPARPAEATSLEGALSTRHSPSVG 300	Qy	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
Db	241 GAAPEPPTPYQGQSMWAHPGTRGPSPDRGFCTVSPARPAEATSLEGALSTRHSPSVG 300	Db	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
Qy	301 ROHHAGPSTSRPSPRMDTPCPVPAIETKFLYSSDKEOLRSPFLLSSLRPSLITGARRL 360	Qy	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
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Qy	361 VETIFLGSRPWMPGTPRPLPRLPQRYWMQRPFLFLLGNAQCPGVLLKTHCPLRAVYT 420	Qy	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
Db	361 VETIFLGSRPWMPGTPRPLPRLPQRYWMQRPFLFLLGNAQCPGVLLKTHCPLRAVYT 420	Db	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
Qy	421 PAAGVCREKPGQSVAAPEEEDTPPRLVQOLLRQHSSPWQYGYFVRACLRLVPGLGWS 480	Qy	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
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Qy	481 RHNERRFPLRNTKKFKISLGHAKLSSLQELTWMKSVRCAWLRSPGVCPAAEHLREBI 540	Qy	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
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Qy	541 LAKEFLHWLMSSYYVVELIRSFFYVTETFOKNRLFFYRKSYNSKLSQIGIQRQLKRVQLRE 600	Qy	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
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Qy	601 LSEAEVQHREARPALLTSURFIPKPDGLRPIVNMDDYVQGARTPRERAERLTSVKA 660	Qy	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
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Qy	661 LFSVNLNTERARRPGLLQASVGLDDIHRATFTVLRVRAOPPPELYFVKVDTGAYDTI 720	Qy	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
Db	661 LFSVNLNTERARRPGLLQASVGLDDIHRATFTVLRVRAOPPPELYFVKVDTGAYDTI 720	Db	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
Qy	721 PQDRLTVIASI1KPKONTCYCVRAYAVVQKAAGHGHYKAFKSHVSTLTDLQPYMROFVAHL 780	Qy	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
Db	721 PQDRLTVIASI1KPKONTCYCVRAYAVVQKAAGHGHYKAFKSHVSTLTDLQPYMROFVAHL 780	Db	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
Qy	781 QETSPLRDVAVTEQSSLINEASSGLDPVLFPMCHAVR.RGKSIVQCGIPQGSLSTL 840	Qy	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
Db	781 QETSPLRDVAVTEQSSLINEASSGLDPVLFPMCHAVR.RGKSIVQCGIPQGSLSTL 840	Db	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
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Qy	901 RKTIVNPFPVEDAEGTATVOMPAHGFPMCGLLDRTTLEYQSDSYARTSTRASLTF 960	Qy	1081 KLTTRHRVTVPLUGSLRTAQTLQRSLKLPGTTLTALEAAANPALPSDFKTLL 1132
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121	SYLPNTVTDLRGSGAWGLLRLRVSDVLLVHLLARCAFLVAPSCAYQVCGPPLYQLGA	180
181	ATQAPPPIASGPRLGCERAWNNSVREAVGPLGPAPGARRGCSASSLPLPKRPRR	240
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361	VETIFLGSRPWWPGTPLLPRLPQYWMRPLFELLNGHAQCPGVLLKTHCPLRAAVT	420
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421	PAAGUCAREPKQGSTVAPEEEEDTDPRLVOLLRQHSSPQWVYGFTRACLRLLVPGLWGS	480
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481	RHNERFLRNLNTKKFISLGKAHKLSIQLETWKMSVRCAWLRSRSPGCVPAAEHLRLREEI	540
481	RHNERFLRNLNTKKFISLGKAHKLSIQLETWKMSVRCAWLRSRSPGCVPAAEHLRLREEI	540
541	LAKPHWLMNSVVYELLRSFYYVTTTFQKNRLFYRKTSWSKLQSIGITRQLKVLQVLR	600
541	LAKPHWLMNSVVYELLRSFYYVTTTFQKNRLFYRKTSWSKLQSIGITRQLKVLQVLR	600
601	LSEABVQHREARPALLTSRLRFPKDGLRPINVMDVYVGARTTREKERAELTSRVKA	660
601	LSEABVQHREARPALLTSRLRFPKDGLRPINVMDVYVGARTTREKERAELTSRVKA	660
661	LFSVLYNVEARRPGILGASVYGLDDIHRAWRTFVIRVRAODPPIPFLYFVKVDVTGAYDTI	720
661	LFSVLYNVEARRPGILGASVYGLDDIHRAWRTFVIRVRAODPPIPFLYFVKVDVTGAYDTI	720
721	PQDRITEVASI1KQNTYCVRRYVQVKAAGHHTRKAFSHVSTLTDQPYMRDFV AHL	780
721	PQDRITEVASI1KQNTYCVRRYVQVKAAGHHTRKAFSHVSTLTDQPYMRDFV AHL	780
781	QETSPLRDVAVIEQSSSLNEASSGLFDVFLRPMCHAVRJRGKSYVQCGJPOGSILSTL	840
781	QETSPLRDVAVIEQSSSLNEASSGLFDVFLRPMCHAVRJRGKSYVQCGJPOGSILSTL	840
841	LCSLICGDMEALKLPGAIRDGLLRLVDDFLVTHPLTHAKTFLTFLVRLGVPYECV VNL	900
841	LCSLICGDMEALKLPGAIRDGLLRLVDDFLVTHPLTHAKTFLTFLVRLGVPYECV VNL	900
901	RKTVNPFYDEAIGTAFQMPAGLFPWCKLQVNSLCTQVTCMNYKILLQAYRFHACV LQLP	1020
901	RKTVNPFYDEAIGTAFQMPAGLFPWCKLQVNSLCTQVTCMNYKILLQAYRFHACV LQLP	1020
961	NRGPAGRMNRKLFQYLRLKCHSFLDLDQVNSLCTQVTCMNYKILLQAYRFHACV LQLP	1080
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1021	FHQQWKNPTEFLRVISDPLCYSLKAKNAGMSIGAKAAGGPSEAVQWLQHQAFL	1132
1021	FHQQWKNPTEFLRVISDPLCYSLKAKNAGMSIGAKAAGGPSEAVQWLQHQAFL	1132
1081	KLTRHRVTVPLGSSLRATQOSRKLPGTTLTALEAAANPALPDKFTLID	1132
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RESULT 9  
US-10-054-611-225

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; Sequence 225, Application US10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;           Lingner, Joachim
;           Nakamura, Toru
;           Chapman, Karen B.
;           Morin, Gregg B.
;           Harley, Calvin
;           Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Townsend and Townsend & Associates, Inc.
; STREET: Two Embarcadero Center
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/Windows
; SOFTWARE: PatentIn Release 3.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US10054611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/855,225
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/855,225
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/855,225
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/855,225
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REFERENCE/DOCKET NUMBER: 36,4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 225:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 225
; US-10-054-611-225

Query Match 100.0% Score 100.0%
Best Local Similarity 100.0% Pred 0
Matches 1132; Conservative 0; Mi 0

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1 MPRAPCRAYRSLLRSHYREVYLPLA
61 DARPPPAAPSPFQVSCLKELYVARVLC
61 DARPPPAAPSPFQVSCLKELYVARVLC
61 DARPPPAAPSPFQVSCLKELYVARVLC
121 SYLPTVTDALRGSGWGLLRRVGIC
121 SYLPTVTDALRGSGWGLLRRVGIC
181 ATQARPYPHASGPRLGCERAWH
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301	ROHHGPPSTSRRPPWDTCPVVAETKFLYSSGDKEOLRPSLSSRLPSTLGARRL	360
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361	VETIFLGSRWMMPGPRLPRLPQRYWQMPRLPFLLEILGNHAQCPYCVLLKTHCPRAAVT	420
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421	PAAGGCAREKPGQSVAAPEEEDTDPLRLVQLRQISSPWQYGFTRACLRVLVPGLWGS	480
	421 PAAGGCAREKPGQSVAAPEEEDTDPLRLVQLRQISSPWQYGFTRACLRVLVPGLWGS	480
481	RHNEERFLRNTKFSIGKHAKLSQLELTWKMSVRCAMLRLRSPVGCVPAEHREIEI	540
	481 RHNEERFLRNTKFSIGKHAKLSQLELTWKMSVRCAMLRLRSPVGCVPAEHREIEI	540
541	LAKFHLWLMSSYYVELLRSFFYTETTFOQRNLFFYRKSYWSKLSQSIGIQLKRVQRL	600
	541 LAKFHLWLMSSYYVELLRSFFYTETTFOQRNLFFYRKSYWSKLSQSIGIQLKRVQRL	600
601	LSEAVRQHREARPALTSRSLRFKPDGLRPIVNDYVVGARTPRKEAERLTSRVRKA	660
	601 LSEAVRQHREARPALTSRSLRFKPDGLRPIVNDYVVGARTPRKEAERLTSRVRKA	660
661	LFSVINYERARRPGCLGASVIGLDIHDRAWRTFVLRVRAODPPELYFVKVDTGAYDTI	720
	661 LFSVINYERARRPGCLGASVIGLDIHDRAWRTFVLRVRAODPPELYFVKVDTGAYDTI	720
721	PQRDTEVIASI IKQONTYCVRAYAVVQKAHGHYTKAFSHVSTLTLDQYPMRQFVAHL	780
	721 PQRDTEVIASI IKQONTYCVRAYAVVQKAHGHYTKAFSHVSTLTLDQYPMRQFVAHL	780
781	QETSPLRDVAVIIEQSSLNBAASSGLFDVFRLFMCHHAVRIGKSYTQCGQTPOGSILSTL	840
	781 QETSPLRDVAVIIEQSSLNBAASSGLFDVFRLFMCHHAVRIGKSYTQCGQTPOGSILSTL	840
841	ICSIYCGDMENKLFIGIRRGQLLFLYDDPELVPHLTHAKTFELTLVRSYPEYCSVNL	900
	841 ICSIYCGDMENKLFIGIRRGQLLFLYDDPELVPHLTHAKTFELTLVRSYPEYCSVNL	900
901	RKTVNFPVEDBALGGTAFQMPAIGLPFWQGLLIDLTLEVQSYSSYARTSIASLTF	960
	901 RKTVNFPVEDBALGGTAFQMPAIGLPFWQGLLIDLTLEVQSYSSYARTSIASLTF	960
961	NRGFFAGRMRKLFQYRLKCHSFLDLOVNSLQTCNTYKILLQAYRFHACVQLQLP	1024
	961 NRGFFAGRMRKLFQYRLKCHSFLDLOVNSLQTCNTYKILLQAYRFHACVQLQLP	1024
1021	FHQQTWKNPFFLRTISDPLSILCYSILKARNAGMISLGAKAAGGPPSEAYQWLQCHQAFL	1084
	1021 FHQQTWKNPFFLRTISDPLSILCYSILKARNAGMISLGAKAAGGPPSEAYQWLQCHQAFL	1084
1081	KLTRHRVTYPLLGSLRATAQQLSRLKPGTTLTALEAAANPALPSDFKTIID	1132
	1081 KLTRHRVTYPLLGSLRATAQQLSRLKPGTTLTALEAAANPALPSDFKTIID	1132
1081	KLTRHRVTYPLLGSLRATAQQLSRLKPGTTLTALEAAANPALPSDFKTIID	1132

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1132 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-10-044-692-2

Query Match	100.0%	Score 5961;	DB 14;	Length 1132;
Best Local Similarity	100.0%	Pred. No. 0;	Indels 0;	Gaps 0;
Matches 1132;	Conservative 0;	Mismatches 0;		

1 MPPAPRCAVRSLRSHYREVPLATFVRLGPQGWLRVQRGDPAAFLVAQCLVCYVFW 60  
 1 MPPAPRCAVRSLRSHYREVPLATFVRLGPQGWLRVQRGDPAAFLVAQCLVCYVFW 60

61 DARPPPAAPSPROVSCKELKLYARVQLQLCERAKNVLAFGFALLDARGPPAFTSTYR 120  
 61 DARPPPAAPSPROVSCKELKLYARVQLQLCERAKNVLAFGFALLDARGPPAFTSTYR 120

61 SYLPNTTDAIGSGANGLLRRVGDDLVHLARCLFVLVAPSCKAVQCGPPLYQLG 180  
 61 SYLPNTTDAIGSGANGLLRRVGDDLVHLARCLFVLVAPSCKAVQCGPPLYQLG 180

181 ATQARPYPHASGPRRRLGCERAWHNSYREAGYVBLGLPAGGARRGGASRSLPLPKRPRR 240  
 181 ATQARPYPHASGPRRRLGCERAWHNSYREAGYVBLGLPAGGARRGGASRSLPLPKRPRR 240

241 GAAPEPRTPVQGQSWAHPGRTGPSPDRGFCVYSPARPAEATSLEGALSCTRHSHPSYG 300  
 241 GAAPEPRTPVQGQSWAHPGRTGPSPDRGFCVYSPARPAEATSLEGALSCTRHSHPSYG 300

241 RQHAGGPSTSPRPPDTPCPVPPVAYETKFLYSSGKEQLRPSFLSSLRPSLTGARL 360  
 241 RQHAGGPSTSPRPPDTPCPVPPVAYETKFLYSSGKEQLRPSFLSSLRPSLTGARL 360

361 VETIFLSSRPWMPGTTPRPLPRLPQRWYQMRPLPFLLELGNHAOCPYGYLLKTHCPLRAAVT 420  
 361 VETIFLSSRPWMPGTTPRPLPRLPDRQYQMRPLPFLLELGNHAOCPYGYLLKTHCPLRAAVT 420

361 PAAGYCAREPKQGSVAPEEEEDTDPRIVOLIQRHSSPWOQYGYVRACLRLVPPGLNGS 480  
 361 PAAGYCAREPKQGSVAPEEEEDTDPRIVOLIQRHSSPWOQYGYVRACLRLVPPGLNGS 480

481 RHNERRFLRNTKKFISIGKHKLSQLTWKMSVRDCAWLRSRSPGVPAAEHRLREI 540  
 481 RHNERRFLRNTKKFISIGKHKLSQLTWKMSVRDCAWLRSRSPGVPAAEHRLREI 540

541 LAKFLHLMSYVVELLRSFPVTTETFQKQNLFFYTKSVWSKLQSIGRQLKRVQRLRE 600  
 541 LAKFLHLMSYVVELLRSFPVTTETFQKQNLFFYTKSVWSKLQSIGRQLKRVQRLRE 600

601 LSEAEVYRQHREARPALTSRLRFPKPDGLRPIVNMDDYVGARTFREKRAEFTSRYKA 660  
 601 LSEAEVYRQHREARPALTSRLRFPKPDGLRPTVNMDDYVGARTFREKRAEFTSRYKA 660

661 LFSVNLNEYRARPGLGASVGLDDIFRAWTTFVLRVRAQDPPELNVFKVDVTGADTI 720  
 661 LFSVNLNEYRARPGLGASVGLDDIFRAWTTFVLRVRAQDPPELNVFKVDVTGADTI 720

721 PDRLTIVIASIKPQNTCYCYYAVVQKAAGHVRKAFKSHVSTLTDQPYMRFQYPAHL 780  
 721 PDRLTIVIASIKPQNTCYCYYAVVQKAAGHVRKAFKSHVSTLTDQPYMRFQYPAHL 780

781 QETSPIRDAVVEIQSSNLNEASSGLPFDYFLPFMCMBVRTRCKSYVCCGQIPGQSTLSTL 840  
 781 QETSPIRDAVVEIQSSNLNEASSGLPFDYFLPFMCMBVRTRCKSYVCCGQIPGQSTLSTL 840

841 LCSLCYGDMDENKLFAIGTRDGILLRVDDELLVTPPHITAKTFLRTLVGPEYGVNL 900  
 841 LCSLCYGDMDENKLFAIGTRDGILLRVDDELLVTPPHITAKTFLRTLVGPEYGVNL 900

841 LCSLCYGDMDENKLFAIGTRDGILLRVDDELLVTPPHITAKTFLRTLVGPEYGVNL 900  
 841 LCSLCYGDMDENKLFAIGTRDGILLRVDDELLVTPPHITAKTFLRTLVGPEYGVNL 900

961 RKTIVNNPVEDALGGTAFVNPAHGLPWPMSGILLDTRTLEVSDYSSYARTSIRASLTW 900  
 961 RKGKAGRNMRRMKLFGVURLKCHSLFELDQNSLOTCTNLYKILLQAYRHACVQLP 1020  
 961 RKGKAGRNMRRMKLFGVURLKCHSLFELDQNSLOTCTNLYKILLQAYRHACVQLP 1020

1021 FHQQWNKPTFFRVISDASLICSYSLIKAKAGMSLGAKGAGPLPSEAVWLNCHOAFL 1080  
 1021 FHQQWNKPTFFRVISDASLICSYSLIKAKAGMSLGAKGAGPLPSEAVWLNCHOAFL 1080

1081 KLTZRHRVTVYVPLLSRITAQTOSLSRKLPGTITLTAEAANPALSDFKTIID 1132  
 1081 KLTZRHRVTVYVPLLSRITAQTOSLSRKLPGTITLTAEAANPALSDFKTIID 1132

ISUULT 11

Sequence 2, Application US/10044-692  
 Publication No. US20030096344A1  
 GENERAL INFORMATION:  
 APPLICANT: Cech, Thomas R.  
 Lingner, Joachim  
 Nakamura, Toru  
 Chapman, Karen B.  
 Morin, Gregg B.  
 Harley, Calvin  
 Andrews, William H.  
 TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS  
 NUMBER OF SEQUENCES: 335  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, 8th Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States of America  
 ZIP: 94111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/044,692  
 FILING DATE: 11-Jan-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/912,951  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: US 08 / 854, 050  
 FILING DATE: 09-MAY-997  
 APPLICATION NUMBER: US 08 / 851, 043  
 FILING DATE: 06-MAY-1997  
 APPLICATION NUMBER: US 08 / 846, 017  
 FILING DATE: 25-APR-1997  
 APPLICATION NUMBER: US 08 / 844, 419  
 FILING DATE: 18-APR-1997  
 APPLICATION NUMBER: US 08 / 724, 643  
 FILING DATE: 01-OCT-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Apple, Randolph T.  
 REGISTRATION NUMBER: 36,429  
 TELECOMMUNICATION INFORMATION:  
 TELEFAX: (415) 576-0200  
 INFORMATION FOR SEQ ID NO: 2:

901 RKTIVNNPVEDALGGTAFVNPAHGLPWPMSGILLDTRTLEVSDYSSYARTSIRASLTW 900

RESULT 12  
US-10-044-519-2  
Sequence 2, Application US/10044519  
; Publication No. US20030100093A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Moin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS  
NUMBER OF SEQUENCES: 335  
CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-POS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/044,539  
; FILING DATE: 11-Jan-2002  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/912,951  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002600US  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEX/FAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1132 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
; US-10-044-539-2  
Query Match 100.0%; Score 5961; DB 14; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MPRAPCRAVRSLLSRYREVLPATFVRLLGPQQWRLVORGDPAAFRALVAQCLYCVPW 60  
Db 1 MPRAPCRAVRSLLSRYREVLPATFVRLLGPQQWRLVORGDPAAFRALVAQCLYCVPW 60  
Qy 61 DARPPAAPSPRSVQSCSKELVARTLQLRCERGAKVNLAFGFLDARGGPPEAFTSVR 120  
Db 61 DARPPAAPSPRSVQSCSKELVARTLQLRCERGAKVNLAFGFLDARGGPPEAFTSVR 120  
Qy 121 SYLPNTVTDALRGSGAWGLLRLRVEDDVYLHLLARCALFYLVAPSCAYQVCGPPIYQOLGA 180  
Db 121 SYLPNTVTDALRGSGAWGLLRLRVEDDVYLHLLARCALFYLVAPSCAYQVCGPPIYQOLGA 180  
Qy 181 ATQARPPHASGPRRLGCRAMWHSVREAGYPLGPAPGARRGGSAERSLPLPKRPRR 240  
Db 181 ATQARPPHASGPRRLGCRAMWHSVREAGVPLGPAPGARRGGSAERSLPLPKRPRR 240  
Qy 241 GAAPEPERTPVQGSWAHPGRTRGSDRGRCVSPARPAEATSLEGALSGTRSHPSVG 300  
Db 241 GAAPEPERTPVQGSWAHPGRTRGSDRGFCVSPARPAEATSLEGALSGTRSHPSVG 300  
Qy 301 RQHAGGPPSPSRSPRPWDTCPYCPPYAETKHFLYSSGDKEQLRSPSFLSSURPSLTGARRL 360  
Db 301 RQHAGGPPSPSRSPRPWDTCPYCPPYAETKHFLYSSGDKEQLRSPSFLSSURPSLTGARRL 360  
Qy 361 VETITFGSRPMPGTPRRPLPQYQWQPLFLIGLNAQCPYGVLLKTHCPLRAAVT 420  
Db 361 VETITFGSRPMPGTPRRPLPQYQWQPLFLIGLNAQCPYGVLLKTHCPLRAAVT 420  
Qy 421 PAAGYCAREKPGSYVAAPEEEEDTDPRLVOLLQHSSPWQVYGFYTRACLRLVPPLGWS 480  
Db 421 PAAGYCAREKPGSYVAAPEEEEDTDPRLVOLLQHSSPWQVYGFYTRACLRLVPPLGWS 480  
Qy 481 RHNERERFLRTKKFISLGKHAKLSQLQELTMWSRDCAWJRSRPGVGCYPAAEHLREEI 540  
Db 481 RHNERERFLRTKKFISLGKHAKLSQLQELTMWSRDCAWJRSRPGVGCYPAAEHLREEI 540  
Qy 541 LAKFLHMLMSVYVWLLSPYTTETTFOQNRLLFYRKSTWMSLQSIGIQLHLKRVQLRE 600  
Db 541 LAKFLHMLMSVYVWLLSPYTTETTFOQNRLLFYRKSTWMSLQSIGIQLHLKRVQLRE 600  
Qy 601 LSEAETQRHREARPALLTSRLRFIPKPDGIRPPIVMDYVUGARTPRREKAERLSRVKA 660  
Db 601 LSEAETQRHREARPALLTSRLRFIPKPDGIRPPIVMDYVUGARTPRREKAERLSRVKA 660  
Qy 661 LFSVINYERARRPGLGASVGLDDIHRARVTFVLRVRAODPPPELYFVKVDVTGAYDTI 720  
Db 661 LFSVINYERARRPGLGASVGLDDIHRARVTFVLRVRAODPPPELYFVKVDVTGAYDTI 720  
Qy 721 PQDLTEVISIILKQNTCYRRAVQOKAHGHYKAFKSHVSILTDLQPYMRFQV AHL 780  
Db 721 PQDLTEVISIILKQNTCYRRAVQOKAHGHYKAFKSHVSILTDLQPYMRFQV AHL 780  
Qy 781 QETSPLRDAVVIQESSLNEASSGLEDFVLFMCHHAVRTRGKSTVQCGQIPQGSILSTL 840  
Db 781 QETSPLRDAVVIQESSLNEASSGLEDFVLFMCHHAVRTRGKSTVQCGQIPQGSILSTL 840  
Qy 841 LCSLCYGDMEKLFAIGIRDGLLRLVDDFLVTPHLTHAKTFKRLTYVGPYEGCVVNL 900  
Db 841 LCSLCYGDMEKLFAIGIRDGLLRLVDDFLVTPHLTHAKTFKRLTYVGPYEGCVVNL 900  
Qy 901 RKTIVNFNPVEDEALGSTAFQMPANGLPNCGLLDTRTLVEQSDYSSYARTSIRASLTTF 960  
Db 901 RKTIVNFNPVEDEALGSTAFQMPANGLPNCGLLDTRTLVEQSDYSSYARTSIRASLTTF 960  
Qy 961 NRGFKAGRNNRKLFGLVRLKCHSLFLDQYNSLQTVCTNLYKLLQAYRFHACVLQLP 1020

RESULT 14  
US-10-325-810-2  
Sequence 2, Application US/10325810  
; Publication No. US20030204069A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joichim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
CITY: California  
COUNTRY: USA  
ZIP: 94111-3034  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/325,810  
FILING DATE: 20-Dec-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:



Qy 1 MPRAPRCAVRSLRLSHYREVPLATFVRRGPGQHVLVQGDPAAFRALVAOCLVCVPW 60  
 Db 1 MPRAPRCAVRSLRLSHYREVPLATFVRRGPGQHVLVQGDPAAFRALVAOCLVCVPW 60

Qy 61 DARPPAAPSFRQSCLEKYLARVLQLRCERGAKNVLAFCGFALLDARGGPEAFTTSVR 120  
 Db 61 DARPPAAPSFRQSCLEKYLARVLQLRCERGAKNVLAFCGFALLDARGGPEAFTTSVR 120

Qy 121 SYLPNTTDDALRGSGAWGLLRRVGDDVLLHLARCAFLVAPSCAYQVCGPPEYQLGA 180  
 Db 121 SYLPNTTDDALRGSGAWGLLRRVGDDVLLHLARCAFLVAPSCAYQVCGPPEYQLGA 180

Qy 181 ATQARPDPHASPRRIGCERAWNHSREAGVPLGLPAPGARRGGASRSLPLPKPRR 240  
 Db 181 ATQARPDPHASPRRIGCERAWNHSREAGVPLGLPAPGARRGGASRSLPLPKPRR 240

Qy 241 GAPEPERTPYCGQGSWAHPGRGTPSDRGFCVVSAPPABEATSLEGALSGTRISHPSVG 300  
 Db 241 GAPEPERTPYCGQGSWAHPGRGTPSDRGFCVVSAPPABEATSLEGALSGTRISHPSVG 300

Qy 301 RQHHAGGPSTERPPWDTPCPVYAAETKHFLYSSGDKEOLRSPSLSSLRPLTGARRL 360  
 Db 301 RQHHAGGPSTERPPWDTPCPVYAAETKHFLYSSGDKEOLRSPSLSSLRPLTGARRL 360

Qy 361 VETIFLGSRPRMPGTPRPLPRLPQLQWQMPLFLLELGENAQCPYGVLKTHCPLRAAVT 420  
 Db 361 VETIFLGSRPRMPGTPRPLPQLQWQMPLFLLELGENAQCPYGVLKTHCPLRAAVT 420

Qy 421 PAAGYCAREKFGSYAAPEEEEDTDPRLVOLLRHSSPWQYGYFRACRLRLYPGWLNGS 480  
 Db 421 PAAGYCAREKFGSYAAPEEEEDTDPRLVOLLRHSSPWQYGYFRACRLRLYPGWLNGS 480

Qy 481 RHNERFLRNTKFKFISKGKAHLSQLETWMSYRDCAANLRSRGVGCYPAABERLREBI 540  
 Db 481 RHNERFLRNTKFKFISKGKAHLSQLETWMSYRDCAANLRSRGVGCYPAABERLREBI 540

Qy 541 LAKFLHWLMSTYVVLLRSFYYVTTETFOKNRLFFYRKSYWMSKLQS1GTRQHJKRVORE 600  
 Db 541 LAKFLHWLMSTYVVLLRSFYYVTTETFOKNRLFFYRKSYWMSKLQS1GTRQHJKRVORE 600

Qy 601 LSEAETRQHREARPALLTSRLFIPKPDGLRPVNMDDYUFGARTFRREKRAERLTTSVKA 660  
 Db 601 LSEAETRQHREARPALLTSRLFIPKPDGLRPVNMDDYUFGARTFRREKRAERLTTSVKA 660

Qy 661 LFSVINYERARRPGLGASYVGLDDIHRRAWTFVLRVQDPPPELYFKVDVTGAYTI 720  
 Db 661 LFSVINYERARRPGLGASYVGLDDIHRRAWTFVLRVQDPPPELYFKVDVTGAYTI 720

Qy 721 PDRLTEVIASTIKPONTYCVRRAYVOKAAAHGHVKAFKSHYSTLTDQPMYRQFY AHL 780  
 Db 721 PDRLTEVIASTIKPONTYCVRRAYVOKAAAHGHVKAFKSHYSTLTDQPMYRQFY AHL 780

Qy 781 QETSPSLRADVIEQSSSLNEASSGLFDVLFRMCHHARVIRGKSYVOOGIPOGSILSTL 840  
 Db 781 QETSPSLRADVIEQSSSLNEASSGLFDVLFRMCHHARVIRGKSYVOOGIPOGSILSTL 840

Qy 841 LCSLCYGDMDENKLFAIGIRGGLLRLVDDFLLYTHLTHAKTEFLTRVQPEYGCYVNL 900  
 Db 841 LCSLCYGDMDENKLFAIGIRGGLLRLVDDFLLYTHLTHAKTEFLTRVQPEYGCYVNL 900

Qy 901 RKTIVNPFYVEDEALGTAFYQMPAHGLFPWCGJLJDRTITLEVQSDYSSYARTSIRASITF 960  
 Db 901 RKTIVNPFYVEDEALGTAFYQMPAHGLFPWCGJLJDRTITLEVQSDYSSYARTSIRASITF 960

Qy 961 NRGFKAAGRNNMRKLFGVNLKCHSLFJLDQNSLQTCTN1KILLQAYRPHACVQLP 1020  
 Db 961 NRGFKAAGRNNMRKLFGVNLKCHSLFJLDQNSLQTCTN1KILLQAYRPHACVQLP 1020

Qy 1021 FHQQTWNQNPFLRVISDASLCTSILKAKNAGNSLGFKGAAGPLPSAVQMLCHOAFL 1080  
 Db 1021 FHQQTWNQNPFLRVISDASLCTSILKAKNAGNSLGFKGAAGPLPSAVQMLCHOAFL 1080

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OM protein - protein search, using sw model

Run on: January 10, 2005, 17:23:35 ; Search time 50 Seconds  
 (without alignments)  
 2178.348 Million cell updates/sec

Title: US-10-053-758-225  
 Perfect score: 5961  
 Sequence: 1 MPRAPRCAVRSLRSHRE . . . . . TALEAAANPALPSDFKTLID 1132

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR 79.\*  
 1: pir1.\*  
 2: pir2.\*  
 3: pir3.\*  
 4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5961	100.0	1132	2 T03844	telomerase catalyst
2	724.5	12.2	1123	2 T51517	telomerase reverse telomerase catalyst
3	594.5	10.0	989	2 T03838	telomerase reverse telomerase (EC 2.7)
4	395	6.6	1132	2 T31107	telomerase catalyst
5	363	6.1	1117	2 T14891	unconventional myo BHFLI protein - hu
6	356.5	6.0	984	2 S53396	unconventional myo BHFLI protein - hu
7	176.5	3.0	3530	2 A59266	hypothetical prote
8	172.5	2.9	660	1 Q0BE3	hypothetical prote
9	144	2.4	3511	2 A59295	immediate early pr
10	142.5	2.4	1560	2 T00080	ABC transporter, A
11	140.5	2.4	1892	2 T18314	gene LF3 protein -
12	140	2.3	1460	1 EDBEIF	N-methyl-D-asparta
13	139.5	2.3	552	2 F75311	inositol 1,4,5-tri
14	138.5	2.3	924	2 S27923	orotidine 5'-phosp
15	135	2.3	1356	2 C45219	hypothetical prote
16	134.5	2.3	946	2 JC7810	RNA-directed DNA p
17	134	2.2	606	2 G75302	atrophin-1 - human
18	133	2.2	1106	2 J00405	immediate early pr
19	132	2.2	860	2 S55543	atrophin-1 - human
20	131.5	2.2	1184	2 G01763	atrophin-1 - human
21	131	2.2	1446	1 A45344	inositol 1,4,5-tri
22	130.5	2.2	1184	2 S50832	orotidine 5'-phosp
23	130.5	2.2	2715	2 T13049	hypothetical
24	129.5	2.2	383	2 S32975	RNA-directed DNA p
25	129	2.2	403	2 S52796	protein TSE21.13 [
26	129	2.2	1776	2 G86280	hypothetical prote
27	128.5	2.2	628	2 S01955	adenine deaminase-
28	128	2.1	376	2 C75580	C-terminal domain-
29	127.5	2.1	1048	2 T31425	

## ALIGNMENTS

RESULT 1					
T03844	telomerase catalytic chain - human				
N;Alternative names: telomerase reverse transcriptase					
C;Species: Homo sapiens (man)					
C;Accession: T03844					
R;Xantharia, T.M.; Marin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J	Science 277, 955-959, 1997				
A;Title: Telomerase catalytic subunit homologs from fission yeast and human.					
A;Reference number: Z15111; PMID:9740623; PMID:9252327					
A;Accession: T03844					
A;Status: preliminary; translated from GB/EMBL/DBJ					
A;Molecule type: mRNA					
A;Residues: 1-1132 <NAK>					
A;Cross-references: UNIPROT:Q14746; EMBL:AF015950; PIDN:9230016; PIDN: AAC51672.1; PID:9					
A;Experimental source: kidney					
C;Genetics:					
A;Gene: TRT					
A;Map position: 5p					
Query Match	100.0%	Score 5961;	DB 2;	Length 1132;	
Best Local Similarity	100.0%	Pred. No. 0;	Mismatches 0;	Indels 0;	Gaps 0;
Matches 1132; Conservative 0;					

RESULT 1					
1 MPRAPRCAVRSLLRSHYREVPLATEFVRLGPQWRLYORGDPAAFRALVAQCLVCVPW	60	1 MPRAPRCAVRSLLRSHYREVPLATEFVRLGPQWRLYORGDPAAFRALVAQCLVCVPW	60	1 MPRAPRCAVRSLLRSHYREVPLATEFVRLGPQWRLYORGDPAAFRALVAQCLVCVPW	60
Db		Db		Db	
61 DARPDDAAPFPRQSCLELVALVYQRLCERGANVNLAFALLDGARGGPPEAFTTSVR	120	61 DARPDDAAPFPRQSCLELVALVYQRLCERGANVNLAFALLDGARGGPPEAFTTSVR	120	61 DARPDDAAPFPRQSCLELVALVYQRLCERGANVNLAFALLDGARGGPPEAFTTSVR	120
Qy		Qy		Qy	
62 SYLPNTVTDALRGSGAWGLLRLYQRLCERGANVNLAFALLDGARGGPPEAFTTSVR	120	62 SYLPNTVTDALRGSGAWGLLRLYQRLCERGANVNLAFALLDGARGGPPEAFTTSVR	120	62 SYLPNTVTDALRGSGAWGLLRLYQRLCERGANVNLAFALLDGARGGPPEAFTTSVR	120
Db		Db		Db	
63 ATQARPPPHASGPRRLGGERANHNSVREAGVPLVGLPAPGARRGGSASRSLSLPLPKRPRR	240	63 ATQARPPPHASGPRRLGGERANHNSVREAGVPLVGLPAPGARRGGSASRSLSLPLPKRPRR	240	63 ATQARPPPHASGPRRLGGERANHNSVREAGVPLVGLPAPGARRGGSASRSLSLPLPKRPRR	240
Qy		Qy		Qy	
64 GAAPBEPERTVQGSGWAHPPTRGSDRGFCVVSPARPAEBATLEGALSQTRISHPSVG	300	64 GAAPBEPERTVQGSGWAHPPTRGSDRGFCVVSPARPAEBATLEGALSQTRISHPSVG	300	64 GAAPBEPERTVQGSGWAHPPTRGSDRGFCVVSPARPAEBATLEGALSQTRISHPSVG	300
Db		Db		Db	
65 RQHAGGPSTSRPSPRPWDTPCPYTAETKHFLYSSGDKEOLRPSFLSSLRPSLTGARRL	360	65 RQHAGGPSTSRPSPRPWDTPCPYTAETKHFLYSSGDKEOLRPSFLSSLRPSLTGARRL	360	65 RQHAGGPSTSRPSPRPWDTPCPYTAETKHFLYSSGDKEOLRPSFLSSLRPSLTGARRL	360
Db		Db		Db	
66 301 VETIFLGSRPWRMPGTPLLPRPLPQWYQWMPRLPLELLGNHAQCPYGULLKTHCPURAAT	420	66 301 VETIFLGSRPWRMPGTPLLPRPLPQWYQWMPRLPLELLGNHAQCPYGULLKTHCPURAAT	420	66 301 VETIFLGSRPWRMPGTPLLPRPLPQWYQWMPRLPLELLGNHAQCPYGULLKTHCPURAAT	420
Qy		Qy		Qy	
67 361 VETIFLGSRPWRMPGTPLLPRPLPQWYQWMPRLPLELLGNHAQCPYGULLKTHCPURAAT	420	67 361 VETIFLGSRPWRMPGTPLLPRPLPQWYQWMPRLPLELLGNHAQCPYGULLKTHCPURAAT	420	67 361 VETIFLGSRPWRMPGTPLLPRPLPQWYQWMPRLPLELLGNHAQCPYGULLKTHCPURAAT	420



QY	971	RRKLFGVLRKXHSFLDLQVNSLQTVCNTNYKILLQAYRFHACVLQLPFHQQWK-NP	1029	Db	201	RTIETTSITONKSARK-----EVSW-----	219
Db	965	RQKLFCYFLPKCHPLFDNSNIGEVLRLNITYQITFLAANKFHCYTVYEV--SRFWKLHP	1021	Qy	286	EGALGSTRHS--HPSVGROFHAGPPSTSRPRPDTCPVVYAYETRHF-LYSSGDKEQLR	342
Qy	1030	TFFLRVISDTPASLCYSTILKARNAGMSLAGKAAGAQLSEAVQMLQHAQAFLLKUTTRHRT	1089	Db	220	-NSISISRSRFSIFYRSYKK-----FKQDLYENLHSICDRNTVH	256
Db	1022	QTLFRPTITSYRMFLINRVRRTNGSSFRVKLYKEEVIWGLDAYIQVULKKKNSR	1081	Qy	343	PSFLUSSLRSLSLTG-----ARRLVETIFLGSRPMGPGRPL---PRLPQRYQMRRPL	392
Qy	1089	YVPLIGSLRTAQTO--LSRKLUPLGTTULALEAAANPAl	1123	Db	257	--MWLQWIFQRFQGLINAFOVKGIVLKVPLBQTAKLHLR	312
Db	1082	YRMLLTYLKSAKHSLSQQLSSEDRYATDRSNSSSL	1118	Qy	393	FLELIGNHACOPGYLKLTHCPLRAATPAAGVACAREKPGSVAAPEEEEDTDPRRLVQLL	452
<b>RESULT 3</b>							
T03838	Telomerase catalytic chain - fission yeast (Schizosaccharomyces pombe)						
N;Alternate names: telomerase reverse transcriptase_1	C;Species: Schizosaccharomyces pombe	C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999	C;Accession: T03838; T03339; T40085	Qy	335	SYSLEPNQVAFLRSJLVRVPKLIWGNQRIFEFLKLSRYESFSLHYLMSNI	394
R;Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.	A;Title: Telomerase catalytic subunit homologs from fission yeast and human.	A;Reference number: Z15111; MUID:97400623; PMID:3252327	A;Accession: T03838	Db	513	SVRDCAWL---RRSPCGVCPAAEHRLLREELTAKPLHLWLMSVVYELLRSFFYVETTFFQ	569
A;Status: preliminary; translated from GB/EMBL/DDBJ	A;Molecule type: DNA	A;Cross-references: UNIPROT:O13339; EMBL:AF015783; NID:92340167; PIDN:AAC49803.1; PID:92	A;Accession: T03839	Qy	395	KI8LEBWLUGKRNKAMCL--SDPEKRQIAFEFVYLWLNFSFIPILQSFFYTBSSDL	452
A;Residues: 1-989 <NAK>	A;Cross-references: EMBL:AF015783; NID:92340167; PIDN:AAC49802.1; PID:92340168	A;Experimental source: strain 972h(-)	A;Accession: T40085	Db	570	KQRLPFYRKVSWSKQSIGIRQHLKRVQVRLSEAEVRQHREARPALTSRLRFIPKPDG	629
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.	A;Status: preliminary; translated from GB/EMBL/DDBJ	A;Accession: T03839	A;Accession: T40085	Qy	453	RNRRTYFRKDWW-KLICRPPTITSRMMEAFKINENNVRDMQ-TKTLPPAVTRLPIPKNT	510
Submitted to the EMBL Data Library, March 1998	A;Cross-references: EMBL:AL02299; PIDN:CA018391.1; GSPPDB:GN00067; SPDB:SPBC29A3.14C	A;Reference number: 221904	A;Accession: T40085	Db	630	LRP1YMDYVVGARTERREKAAELTSRVKALFSTVLYEARPP-----GLLGASVIGL	683
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	Qy	511	FRLTNL-----RKRLFLIKGNSKNMVST--NOTLRPVASILKHLNEESSGI	558
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	Db	684	D---DTHRAWRTPF---VLRVTAQDPPEELYFVKVDVTGADTIPODRLTETVASTIKPQN	737
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	Qy	559	PFNLEYVMKLTFCDDLLKERMFG--RCKFVFVDIKSCYDRIKQMLFRIVKKKLKDPE	616
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	Db	738	TCYVRRYYAVVOKAAGHVKAFKSHVSTLTDQPYMRFQYAHLOETSPLDVIEQSSS	797
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	Qy	617	-FVTKYATH-ATSDRATKQFVSEAFSYDFMVPEKFVQVOLMSKTS--DTLFYDFDVY	671
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	Db	798	LNEASSGLFDVFLRMCHHAVRIGKSYVOCQGIQGSISLSTLSCLGDMENKLPGI	857
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	Qy	672	WTKSSSEIFKMLKELSGHIVKGNQSYLOKVGIIQGSILSSFLCHFHYMEDLIDBEYLTSFT	731
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	Db	858	RRDG-LLLRLYDDFLVPLTHAKTFLTRVQPEYGCVNLFKTVNNFPVEDEALGG	916
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	Qy	732	RKKGSVSLRQVDDFLITVNUKKDKFLNLSLRGERHNESTSLEXTVINFENSGIINN	791
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	Db	917	TAFQMPAHGLFPWCGLLDTRTEV----QSDYSSYARTSIRASLTENRGFKAGRNM	971
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	Qy	792	TFENYESKRR--MPEFGFSVNMRSIDLACPKIDALENSTSVELTKHMGSKSF-----	842
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	Db	972	RKLFGVTLRKHS--LFLOLQVNSLQTCTVCTNIKYI----LLDAY	1010
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	Qy	843	-FYKILRSSLASFAQVFDITHNSKFNSCCNIRGYSMCMRQAY	887
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	Db	854	RESULT 4	
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	T31107	5	PRCRAVSLLSLASHYREVPLATEVRIGPQGMWLVORGDDAFAFLVAQCL-----	55
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	T31107	7	PKSRILR-FLENQYVYLCTUNDYV-----QLVLRGSPASSYSNICERIRSVDQTSFS	57
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	C;Species: Oxytricha trifallax	56	-----YCPWDARPPAPSPRQVSCIK-ELIVARYLQLRCERG--AKNVLAQFGPAL-LD	105
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	C;Accession: T31107	58	IPLHSTVGFDSKPDEGV-QFSSPKCSQSELIANVQMFDESFERRNLIMKGFSMNH	116
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	R;Bryan, T.M.; Speerger, J.M.; Chapman, K.B.; Cech, T.R.	106	GARGGPPPEAFTSVSYLNTVTDALRGSGAWHLIRVGDVYLHLLARCAFVLFVAPS	165
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	Proc. Natl. Acad. Sci. U.S.A. 95, 8479-8484, 1998	117	DERAMHNGVQNDLVSFPTNPYLISLSE-SKOWQLLIEIGSADMAYLSKGSIIFALPND	175
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	R;Bryant, T.M.; Speerger, J.M.; Chapman, K.B.; Cech, T.R.	166	CAYQVCCPLYOLGAATQARPPPHASGRRRLGCERAWNTSVREAGVPLGLPAPGARRG	225
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	Proc. Natl. Acad. Sci. U.S.A. 95, 8479-8484, 1998	176	NYLQTSICPLPK-----SKRK 200	285
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	A;Title: Telomerase reverse transcriptase genes in Tetrahymena thermophila and Oxytricha trifallax	226	GSASRSIPLPKRPRGAAPEPERTPVQGGSWAHPGRTRGSPDRGFCVSPARPAEATSL	
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	A;Text change: 09-Jul-2004			
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	C;Sequence revision: 02-Sep-2000			
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	C;Accession: T31107			
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	R;Bryant, T.M.; Speerger, J.M.; Chapman, K.B.; Cech, T.R.			
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	Proc. Natl. Acad. Sci. U.S.A. 95, 8479-8484, 1998			
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	A;Reference number: Z20985; PMID:98337340; PMID:9671703			
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	A;Accession: T31107			
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	A;Status: preliminary; translated from GB/EMBL/DDBJ			
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	A;Molecule type: DNA			
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	A;Residues: 1-1132  			
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	A;Cross-references: UNIPROT:076332; EMBL:AF060230; PIDN:AA			
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	C;Genetics:			
Submitted to the EMBL Data Library, March 1998	A;Experimental source: strain 972h(-); codmid c29A3	A;Accession: T40085	A;Accession: T40085	A;Gene ID:			

Query Match	6.6%; Score 395; DB 2; Length 1132;	Qy	322 PPVYAAETKHFLLYSQSGDKEQLRPSFLSSLRPSLTCARRLVETIPLGSRWMPGPRLER 381
Best Local Similarity	22.2%; Pred. No. 1e-18;	Matches	136; Conservative 114; Mismatches 305; Indels 58; Gaps 15;
Qy	450 QLLRQHSPWQVYGFVRACIRRLYPPGLWSRHNERFLRNTKKFISLGKHAKLSSLQBLT 509	Db	239 PGFV-KSSEPNYS----EIKKGQFKVQIKQKGQR----FINSDKIKPDPQTQIK 286
Db	451 QLFYEQDQBOISNPLTEFVANVPKNFDEGK-NKKIPNKQKQFVKENRFESFTKISLL 509	Qy	382 --LPQRY----WQMRPFLE--LIGNHACQCPGYULLKTCPLRAAVTPAGVCA 428
Qy	510 WCMSYRDCAWLRSPGVGCPAAFH--PLREELAKELIHWMSVYVELLRSFFYTFET 566	Db	287 KTLKBEYQSKNFSCQEERDIFLEETEKVQNPHINENVJLAKCKL---- 333
Db	510 NKFRYNEVSIL---SFICRKDENKFKFMENENHVFFKVLKWKYEDDLATLARCYFSTEK 565	Qy	429 EKPQGSVAABEEDTDPRRLVQLRQHS----SPWQVYGFVRACL 469
Qy	567 TFOQNRBLFPRYKSVNSKLSQKOSIGTRQHLKRVQRLBESLAEVROHEARPALITSRQFPIK 626	Db	334 -----PENYQSLKSQVKQIYSENKANQOQSCENLFSNLSDYTEDISYKQITNWLRLQI 384
Db	566 AKEYORIIFYKRKNWNMMRLS-DDLHQ-NIKQVEKEMRIFCESQ-NFADGKDRIPK 623	Qy	470 RRLVPGLGNSRHNERRFRFLRTNPKFISLGKHAKLSSLQELTWKMSVRDCAWLRRSPGNGCV 529
Qy	627 PDGLRPIVNMDDVVGARTPRRE----KRAERLTSVYK---ALFSTLYNERARRPGLLG 677	Db	385 QNCVPNQOLLGKK-NFKVFLKLELYEFVQMKRPNENQVLYICFMDVDEWF----v 435
Db	624 GDTFRPIM-----FENRKIPLNQVGKPFQSRMTINNKLQTAHHMMLKNUKSKMFKHSFG 674	Qy	530 PAAEHLR-----REBILAKFLHNMSSVYVYELLRSFFYTTETTFOKNRLFYRKSV 580
Qy	678 ASVGLGDDIHRARWFVLRVRAODPPELYFVQDVUTGAYDTIIPQDLTENIAS---- 731	Db	436 DLKQKFTOKRYTISDKRKLGDJLIVFKINKIVIPVLYNFITEKHEKGSOQFYRKPI 495
Db	675 FAVPNYDDIMKRVENFVORKW-QINSPLFYAMDIKCYDNDCERVNFLQKSMDK 733	Qy	581 W---SKLQSIGI-RQHLLKRVOLRELSEAEVRQHAREARPALLTSRLRTPKDPGLRPVNM 636
Qy	732 -----LIKPCONTYCVRYAVVQKAAGHGVKAFKSHVSTLTDLQPYMRQFV AHLQET 783	Db	496 WKLVSKLTIVKLEENLKEVEEKLIPEDSFQKYPQ----GKURIPKIGSFRPIM- 546
Db	734 EYFLINTFTVLKRNKNIIVERSNPKLPIKQFVYKFK-IGIDGSSYPTLFEILLEDEFND 792	Qy	637 DYVVGARTFRREKAERLTSRVKALFS---VLYNEYEARPPELLGASVFLGLDDIHRAWT 692
Qy	784 SPLRDAYVIEQSSSLNBAASSGLFDFVTRFMCHAVAIRGKSYVQCGQIPQGSILSTLCLS 843	Db	547 -----TFLRKDKQKNQKLNQNLNQSLQVFLRNQKNDLQKMDLGOKIGTSVFDNKQISEKFAQ 599
Db	793 LANKKRTLTIVEQERKKFPKNDLQOPVULKICONNYTFENKIQYKQKMGIPQGLCYSYLSS 852	Qy	693 FVLRVRAADPPELYFVQDVUTGAYDTIIPQDLTENIASIIKPKONTYCVRRYAVVQKAAH 752
Qy	844 JCYGDMENKLFAGIRR-----GLLLRVDDDFLVTPLTHAKTFLRLTYRGVPEX 894	Db	600 FTERWKNGK-REPQLYYYTLDIKKCYDSIDQMKLUNNNFQNSDLIQDIFYFINKYLLFQRNKR 658
Db	853 FYANLLEENALQFLRKSMMDPEKPEINLMLTDDYLMLTTEKNAMLFTEKLQIQLSLN 912	Qy	753 GHYRKAFKSHVSTLTDLQ-----PYM----RQFV AHLQE---- 782
Qy	895 GCVNVNLRTKTVNPFVEBALGSTAFYQ---MPAHLGFPWCCLLIDTRTEVQSYSSYAR 951	Db	659 PLIQQQTNNLSAMEEEBKETNKKPFPKMDNINFPTYFNLKERQLAYSLYDDDDQILQKG 718
Db	913 FFPKFMKCLTKTNFALNQKIGCTNTQDIDSINDLFWHGISIDIKUTIONI-NKIK 971	Qy	783 -----TSPLRDAVYIEQSSSLNNEASSGLFDFVFLRMCHAVIRGKSYVQCGQIPQGSILS 838
Qy	952 TSTRASLTFENRGFKAGNMRRKLFGYVRLKCHSLFLDQVNSLQTVCNTNIYKILLQAYR 1011	Db	719 FKEIQSDDRPFTIVNQDKPRCITKDITHNLKHKHSISQYNTFSNKVFKRKGIPQGLNIS 778
Db	972 EGILCTIUVNMOTNESTLWKKLKSFLMANNISPFKSTINTKOFANTITLSKUYAAEK 1031	Qy	839 TLICSLCYGDMDENKLFAGIRD----GILLRLYDDFLVTPHTAKTFLRLTVRGV 891
Qy	1012 FHACVCLQP-FHQ 1023	Db	779 GVLCSPYFGKLEEVEYTOFLKNAEQONGSTINLMRLTDYLFISDQQNALNLIVQLQNC 838
Db	1032 YVACCQFKEFRFHE 1044	Qy	892 PEYGCUVNLRKTVVN--FPEDEAUGTAGTAFVQMPAHGLFPWCGLLDTTRLEVOSDYSSY 949
Qy		Db	839 NNGNEFENDQKITTFNQFQDYNL--EHFKISUNECOWIGNSIDMNTLEIK--SIQ 892
Qy		Qy	950 ARTSASLASLTENRGFKAGNMRRKLFGVRLKCHSLFLDQ-----QVNSLQTVCTNITY 1002
Db		Db	893 KQTQEBINQINTVASSI-KHLSQKKNQIKR----SLFNUQLDYNPNNTSFGCICRQIX 947
Qy		Qy	1003 --KILLOQAYRFHACVQL----PFHQQVWK--NPFPLRVISDTAS---LCY- 1044
Db		Db	948 HHSKATVMKFVYPMWKFLQIDLKRSQJKSVQYGENTNENFLKQIYTYVEDVKILCYL 1007
Qy		Qy	1045 -----SIIKAKAGMISLGAKGAGPLSEAVOWLCHIA 1077
A;Title:	The reverse transcriptase component of the Tetrahymena telomerase ribonuclease	Db	1008 QFEDIEINSNKEIFFNLYSWIMWDIVSYLKKKKQ----FKGSYLNKL----- 1050
A;Reference:	218252; PMID:98337941; PMID:9671704	Qy	1078 FLLKLTTRHRYVYPL-LGSLRATQQLSRKLPGTTLALEAAANPAPLPSDFKTL 1131
A;Status:	Preliminary; translated from GB/EMBL/DDJB	Db	1051 -LQKIRKSRPFYLLKEGCKSLQLLISQKVKQNLNKELEIEFDLNLNIQDICTLI 1104
A;Molecule type:	mRNA	C;Keywords:	nucleotidyltransferase
A;Residue:	1-111 <COL>	C;Genetics:	SGCS
A;Gene:	TERT	A;Cross-references:	UNIPROT:077448; EMBL:AF061284; PID:93335167; PID: AAC3
A;Genetic code:	SGCS	RESULT 6	S53336
N;Alternate names:	telomerase catalytic chain EST2 - yeast (Saccharomyces cerevisiae)		
C;Species:	Saccharomyces cerevisiae		
C;Date:	05-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004		
C;Accession:	S53396		

R.R.Du, Z.		Submitted to the EMBL Data Library, February 1995	
A. Description: The sequence of <i>S. cerevisiae</i> cosmid 8543.		B. Reference number: S53390	
A. Reference number: S53396		A. Cross-references: UNIPROT:Q006163; EMBL:U20618; NID:9225	
A. Molecular type: DNA		A. Experimental source: strain S288C (AB972)	
C. Genetics:		A. Gene: SGD:ES02; MIPS:YLR318w	
A. Cross-references: SGD:S000310; MIPS:YLR318w		A. Map position: 12R	
Query	Match	6.0%	Score 356.5; DB 2; Length 16; Mismatches 309; In
Best	Local Similarity	22.1%	Pred. No. 3.1e-16;
Matches	167; Conservative	127;	Mismatches 309; In
Dy	329 KHEVYSSGDKEQLRS - FLLSSLRLSITGARRLV -- ETIFL		
Dy	185 KQFH - - - KLNINISSSSFPYSKILPSSSSIKLTDIREALF-		
Dy	384 QRYWMQRPLPE-LIIGNHAQCPYGVILKTHCPLRAATPAVG		
Dy	231 QRLKVRINLTQKLKHKRHLNVSLSNSCIP - - - PLEG		
Dy	443 TDPRRLVQLLQRQHSSPWQYGFVRACLRLVYPPGLWGRSHNER		
Dy	270 ---DLSHLSRQ-SPKERVLKFIVTLQKLQPQEMFGSKKNG		
Dy	503 LSQELTWNMSVRDAWLRSPPGCVPAAEHRLR - EELIAK		
Dy	325 LPFDLSSKKLKLRLFRWL - - - FISDIIWTFKHNFENLNQALIC		
Dy	561 FYVETTFFQKNRLFFYRKSVWSKLOSIGIRQLRVLRELSF		
Dy	381 FYCBEIS - STVTVYFRHDWTNLKLTIPFIVEFYKTY - - - LVE		
Dy	619 SRURFIPKPQDGLRPIVNMDDYYV - - - GARTFRREKRAERLT		
Dy	436 SKMRQIPKCS - - - - NNEFRRIAIAPCRGADEBEEFTIYKENHK		
Dy	673 PGLLGASVLGLDDTHRRAWTFVLRV - RAQDPPELYPKVUDV		
Dy	490 PTSPF-TKIXPTSOQADRIKEFKQRLKKFNNVLPSTLMDQKV		
Dy	731 SIIIFQNTYCVRRAYVQKAAGHYRKAFKSFHVSHTLDCQYHM		
Dy	549 DALKNENGFTVRSQQFPN - TNTGVLKLFLNVNNAVRVPKDY -		
Dy	791 VIEQSSSLNEASSGLFDVFLRFMCHHAVERGKSYVQCGIPOQ		
Dy	590 YIDAVRTVHLNSNQDVINVVMEIIFTALWBDKCYTREDGLFQ		
Dy	850 - ENKLFAGIIRRDFGLLRLYDDEFLYTPHLTHAKTFLRLTVRG		
Dy	650 EFYSEFKASPSQSDTILKLAADDFLISTDQQQVINIKKLANG		
Dy	907 FPVDEDEALGGTAAVMPAHGLFPPWCGLLLDRTRLEYQSDYSSY		
Dy	710 SQSDDT - - - - - VIQFCAMHIHFVKELEWKHSSTM		
Dy	967 GRNNRKRKLFGVYLRLKCHSLSFLDLOQNSLQTCVCTNI - - -		
Dy	749 SKGJFRSLTALENTRISYKRTDNUNNSTNTVLMQ1DHVVKNIS		
Dy	1010 YRFACAVLQOLPFPHQOYWKNPFTPFRLVISDASIC 1043		
Dy	809 MQFH - - - - - SFQRQRIEMTVSGC 826		

unconventional myosin-15 - human	C Species: Homo sapiens (man)
	C Date: 02-Jun-2000 #text_change 09-Jul-2004
	C Sequence_revision 02-Jun-2000
	C Accession: A59266
Genomics 61, 243-258, 1999	A;Title: Characterization of the human and mouse unconventional myosin XV genes re
Riiang, Y.-A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T. R. an, T.B.; Friedell, R.P.	A;Reference number: A59266; MUID:20021762; PMID:10552926
A;Accession: A59266	A;Status: preliminary / not compared with conceptual translation
A;Molecule type: mRNA	
A;Residues: 1-3530 <LAA>	
A;Cross-references: UNIPROT:Q9UNN7; GB:Ap14094; NID:96224682; PIDN:AAF05903_1; PI	
F:1225-1887/Domain: myosin motor domain homology <MMO>	
Query Match 3.0%; Score 176.5; DB 2; Length 3530;	
Best Local Similarity 20.6%; Pred. No. 0.0041; Indels 475; Gaps 68;	
Matches 263; Conservative 144; Mismatches 392; NTVDALRGSGAWG 138	
Qy 107 ARGGPPEAFFTS -----VRSYLP-----NTVDALRGSGAWG 138	
Db 2313 SREGPKVWFGNSWDSDEDMSTRPQQEHMPKVYLDSDQYSSHQNQDGNTAQRTG-ATH 2371	
Qy 139 LLRARRGVGDVLHLLARCALFWLVAP-----SCAYQVCQCPPLYQLQGAA --- 181	
Db 2372 QESDSLGPAPVKGLDQYLDLSFDPVLYSYGDADLEKPTAAYMRIGGGQPGGGSSGTE 2431	
Qy 182 -TOARPP --PHASGPERRLGCEBRANNHSVRAEGV --PLGLPAPGARRGGGSAS-RSLP 233	
Db 2432 DTPRRPPPKPFPGLDSTLAIQAFPH -KOAVLLARGMTIQTATLQQPQISAAALRSLP 2489	
Qy 234 LPKRPRRGAAPEPERTPVQGGSWAHPGRTRGSPDRGFCCVSPARPAEATSLEGALSGTR 293	
Db 2490 AEKPP---APEAQPTSVGTGPPAKPVLR -----ATPKDPLA----- 2524	
Qy 294 HSHPSVGRQHHAGGPSTSRRPPWDTCPPVYA-----ETHFLYSSGDKEQLRISFL 347	
Db 2525 -----PLAKAPRLPIKPVAAPIVLAQDQASPET----TSPSPBLVRYSTLN 2565	
Qy 348 SSLRPLSITGARRAVETPLFLGSRSPWMPETPRLPRLPRLPQRYWONRP-----LFELIGHN 400	
Db 2566 SEHFPOPT---QQIKNIVYRQYQOPFRGGRPEALRKDGKVKFMRPDHEALMLKGQMTM 2623	
Qy 401 AQCPYG-----VIIK--THCPLRBAATPAAGYCAREKPGQSVAAPEE-EDTDPRRLV 449	
Db 2624 LAAAPGTYOSREAAVLYKPVTSA-REPMSAPTSAL----PSRSLBEPPEELTQTRLHLRI 2677	
Qy 450 --QLRQHSSPQVYGFTR-----ACLR-----RL 472	
Db 2678 NPFFYGYQDAPWKI--FLRKVEFYPKDYSYSHPVQQLDLFLRQLHDTLSEACLRISERDL 2735	
Qy 473 VPPGLWGSRHNNERRFLNNTKCEPLSG-KHAUQLQBTWQMSVRDCAWLRSRSPGVGCPA 531	
Db 2776 RMKALFAQNQ---LDTQKPLVTESKRAVIISTARDTWEV----YFSRFPATPSVGT 2785	
Qy 532 AEHRLREEPLAKFLHNMISVYVVELR-----SFFEYTETTF-QKNR 572	
Db 2815 LEENLAS--EKVILFSAAH---QVTKLVDDFILEBK----- 2867	
Qy 623 IVNDDYVYQGARTFRREKARLTSRVKALFSVLYERA-----RRPLGLGAS----- 679	
Db 2888 --DSDYTVAVRNLPEPD-----LLAFHKGDITHQPLEPRVYSGACVVR 2913	
Qy 680 --VGLGDDIHR----AWRTFVLRVRAQDPPELYFVKVDTGAYD----TIP-QDRLT 726	
Db 2914 RKVYVLEPLRRLRGDPFWRFGTIGRGRFPSEL----VQPAAAPDPLQLTEPGRRAA 2969	
Qy 727 EVIASLIKPontycerry---AVYQKAAGHVVRKAFKSHVSTLTDLOPIMRQFVTLHQ 781	





A;Residues 1-1460 &lt;CHE&gt;

A;Cross-references: UNIPROT:P11675

C;Superfamily: herpesvirus immediate-early protein IE175

C;Keywords: DNA binding; early protein; transcription regulation

Query Match 2.3%; Score 140; DB 1; Length 1460;

Best Local Similarity 24.3%; Pred. No. 0.38; Mismatches 35; Indels 158; Gaps 27;

Matches 114; Conservative 114;

Qy 46 AFRALYVQCLYCPVDPARPPAAPSFRQVSCLKEILVARYQLRCERGAQKVLQLAGFALD 105

Db 704 ACRGVDELRLLPC-PLRPAAPARAALPQACLETTAAL------ALR 746

Qy 106 GARG-GPEE-----AFTTISVRSYLPNTVTDALRGSGAWGLLRLRVGDDLVHLAR 155

Db 747 AIPGAGPAERQQAADSVALVARTVAPLVR/SVDGARAREAW-----TVA 791

Qy 156 CALFLVIAAPSCAYQVCGPPLYQLGAAATQARPPIHGSPPRRRLGCERAVNNH----S 206

Db 792 AALP---APA--APA--NYAGARL---AEAARPGPAPAP----GLPPLWPEQPGLVLVVPAPA 837

Qy 207 VREAGYPLGLIAPG---ARRGGGAEASRSULPKPRGRGAPEERTPYQGGSWAHPERT 262

Db 838 PAAAGAGPSGLQSLGPSPASTKSGETSKSGTGSLSGS-----GYARLPRRR 887

Qy 263 RGPSPDRGFCVVSPP---ARP-AEEATLSRG-ALSGTSHSPSVGRQHAGPPSTSRRP-- 313

Db 888 PGPSARAQQEEAAPRACARRPSGDGEEDEGLSGSALRGDHGHHRD--DEEDRGPRKRSSIG 945

Qy 314 --PRPMDTPCPVYAEKHFYSSGDEKEQIRPSFLSIRPSLTGARRLIVETIFLGSREW 371

Db 946 LGPAP--DPAPALVSSSS--SSSSSEDRLR-----RP-----LGPNPE 980

Qy 372 MPGTPRRLPFLQTYQMRPLFLETIQLNHQCPYGVLLTHCP-----L 415

Db 981 HPADPGCFRRVPG-----ETHTPRPSAAAALAYCPEVARALVDOEVFPBLW 1028

Qy 416 RAAVT--PA--AGVCAKEKPGQSYAAPEEEBDTDPRLVQLRQHSSPQV 461

Db 1029 RPALTFDPAALAHIAAR--RGAAGAP-----LRRRAWMRQTADPEPDY 1069

RESULT 14

S27923

ABC transporter, ATP-binding protein - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: F75311

C;Author: R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.M.; Shen, M.; VanAathoven, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Status: Preliminary

A;Molecule type: DNA

A;Map position: 1

Query Match 2.3%; Score 139.5; DB 2; Length 552;

Best Local Similarity 22.3%; Pred. No. 0.11; Mismatches 38; Indels 233; Gaps 27;

Matches 134; Conservative 134;

C;Genetics:

Qy 132 RGSGAWGLLIRRSGEDDVYLHLLARCALFVLP-----SCAYQVCP 173

Db 24 RGS---RLQFRVSEKSTRFTSTESLFLCILAPGLTLIASSTGSFIHSDFVATTAAPR 80

Qy 174 P----LYQLGAATAQARPPIHASGPRRRG-----C 199

RESULT 13

S27923

Gene LF3 protein - human herpesvirus 4

C;Species: human herpesvirus 4, Epstein-Barr virus

C;Accession: S27923

C;Author: R.Parker, B.D.; Bickner, A.; Satchwell, S.; Farrell, P.J.

C;Submitted to: the EMBL Data Library, August 1990

C;Description: Sequence and transcription of Raji Epstein-Barr virus DNA spanning the B-

A;Reference number: S27923

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 1-924 &lt;PAR&gt;

C;Cross-references: UNIPROT:Q99307; EMBL:M35547; PIDN:AAA45896-1; PID:9330-

C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology

Query Match 2.3%; Score 138.5; DB 2; Length 924;

Best Local Similarity 27.0%; Pred. No. 0.26; Mismatches 136; Indels 55; Gaps 16;

Matches 80; Conservative 25;

C;Genetics:

Qy 179 GAATQAP-----PHASGPRLGCEBRAWHNSVREAGV-----PGLPAPGARRRGCSA 228

Db 26 GAADPAPVGHPAAPPAPGPBPTRLQPA--TPRSGAADPAPVGHPA--APRAPGPE 80

Qy 229 SRSLLPLKPRPRGAAPPAPERTPVQGSWAHNGRTGSPSDRFGCVVSPARPAEATSLGEA 288

Db 81 PRTRQLPATPRRSQAADP-ADPVG-----HPAAPRAPGPBPTRLQPATPRRSQAADPAD 134

Qy 289 LSGRTRSHPSVGRQHDAHP-----PDSR-----PFRWDPTCPVVAETKHFLYSSGD 337

Db 135 PVG----HPAAPRAPGPBPTRLQPATPRRSQAADPVGHPA-----RAPGP 181

Qy      338 KEQLRPSFLSSLRPSLTGARRLVEVIFLGSRPWMPG-TPR-RL-PRLPORYWQMRPLFL 394  
 Db      182 EPTTR----LQPATPRSGAAADPDPVGHPAAPRPEPTEPRQLQATPRSGAAADP--A 235

Qy      395 ELLGNHACQCPYGVLLKTHCPLRAAVTAAAGVCAREKEQGSVAAPEEEEDTPRRLVQ 450  
 Db      236 DPVG-HPAAPRPGPEPRTRLOPATPRSGAAADPDPVGHPAAPRPGPEPRTRLQ 290

---

RESULT 15

C45219 N-methyl-D-aspartate receptor chain NMDA2D-1 - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C;Accession: C45219  
 P;Ishii, T.; Moriyoshi, K.; Sugihara, H.; Sakurada, K.; Kadonani, H.; Yokoi, M.; Akazawa J. Biol. Chem. 268, 2836-2843, 1993  
 A;Title: Molecular characterization of the family of the N-methyl-D-aspartate receptor  
 A;Reference number: A45219; PMID:9315510;  
 A;Accession: C45219  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-1156 <ISH>  
 A;Experimental source: brain  
 A;Note: sequence extracted from NCBI backbone (NCBIP:124264)  
 C;Superfamily: N-methyl-D-aspartate receptor 2D; glutamate receptor homology  
 F;451-879/Domain: glutamate receptor homology <GRH>

Query Match      2.3%; Score 135; DB 1; Length 1356;  
 Best Local Similarity      27.2%; Pred. No. 0.76; Gaps 22;  
 Matches 88; Conservative 16; Mismatches 102; Indels 118; Gaps 22;

Qy      59 PWDARPPAA----PSFRQVSCLKEIVARYLQRLCERGAKNVLAFQALDG----- 106  
 Db      1084 PRRAAPPVCAVLDLEPS-----PSDSDSESLGGASIGGLEPWFWFA 1124

Qy      107 -----ARGGPEAFTTSVRSYLPNTVTDAIRG--SGANGILLRRVGDDVLVHLJARCA 157  
 Db      1125 DFPYPYPERLGPGRWWSV-----DKUGGRAGSWDYLPPRGGP--AWICRHCA 1172

Qy      158 LFVLFAP----SCAYQWC----GPPLYQLGAATQARPPIHASGP---RRRLGGERAWN 204  
 Db      1173 SLELLPPPRHLSCSHDGLGGMWAPP-----PPWAAGPPPRRZRCGCFRPHP 1221

Qy      205 HSVREA-GVPLGLPAPARR--GG-----SASSSL-PLPKRPRGAAPEPEIT-PVG 252  
 Db      1222 HRPRASHRPAAPAHHRHRRAGGGWFPPPAPTSLEDISSRP---CP-PHRTGDTG 1276

Qy      253 QGSWAHPGRTRGSDRCFCVYSP-----ARPAEEATSLEGALSGTRHSHPSVRQHHA 305  
 Db      1277 AGTWAHDGALR-----ISPAWSRYDADAPPTPAAPSVA---GGPGRGAKWT 1324

Qy      306 GPPSTSR----PPR----FWDTPCPP 323  
 Db      1325 GPSWVGDRNGEGRTPGAAASCAP 1348

Search completed: January 10, 2005, 17:39:30  
 Job time : 57 secs

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OM protein - protein search, using sw model

Run on: January 10, 2005, 17:19:31 ; Search time 168 Seconds  
(without alignments)

2417.152 Million cell updates/sec

Title: US-10-053-758-225

Perfect Score: 5961

Sequence: 1 MPRAPRCAVRSLRLSHRE.....TALEAANPALPSDFKTLID 1132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04 : \*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	5961	100.0	1132	2	AAW46957	AAw46957 Human tel
2	5961	100.0	1132	2	AAW90251	Aaw90251 Human cat
3	5961	100.0	1132	2	AY28881	Aay28881 Human tel
4	5961	100.0	1132	2	AYY32050	Ayy32050 Human tel
5	5961	100.0	1132	2	AYY43621	Aayy43621 A human t
6	5961	100.0	1132	2	AYY26580	Aayy26580 Human tel
7	5961	100.0	1132	4	AGG64859	Aagg64859 Heart mus
8	5961	100.0	1132	4	AGG64329	Aagg64329 Human pro
9	5961	100.0	1132	4	AA99930	Aab9930 Human tel
10	5961	100.0	1132	4	AB82755	Aab82755 Human tel
11	5961	100.0	1132	5	AEE9226	Aee9226 Human tel
12	5961	100.0	1132	5	AAU72735	Aau72735 Human tel
13	5961	100.0	1132	6	ABR42384	Abr42384 Human tel
14	5961	100.0	1132	6	ABR2053	Abr2053 Human tel
15	5961	100.0	1132	6	ABP56676	Abp56676 Human tel
16	5961	100.0	1132	6	ABR58045	Abr58045 Human tel
17	5961	100.0	1132	7	ADD21420	Add21420 Human TER
18	5961	100.0	1132	7	ADH72743	Adh72743 Human pro
19	5961	100.0	1132	8	ADG70114	Adg70114 hTERT pro
20	5961	100.0	1132	8	ADG9059	Adg9059 Human TER
21	5961	100.0	1132	8	ADJ82172	Adj82172 Human tel
22	5961	100.0	1154	2	AAW61350	Aaw61350 Human tel
23	5961	100.0	1189	2	AAW47008	Aaw47008 Glutathio
24	5955	99.9	1285	2	AAW47000	Aaw47000 HIS tagge
25	5954	99.9	1132	2	AAW71376	Aaw71376 Human tel

#### ALIGNMENTS

RESULT 1  
AAW46957

standard; protein; 1132 AA.  
AC: AAW46957;

DT: 13-AUG-1998 (first entry)

DE: Human telomerase reverse transcriptase.

XX: Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;

XX: cell proliferation; cancer; ageing; ribonucleoprotein.

XX: Homo sapiens.

XX: PN: Q82317891-A.

XX: PD: 08-APR-1998.

XX: PF: 01-OCT-1997;

XX: PP: 97GB-00020890.

XX: PR: 01-OCT-1996;

XX: PR: 18-APR-1997;

XX: PR: 25-APR-1997;

XX: PR: 06-MAY-1997;

XX: PR: 09-MAY-1997;

XX: PR: 14-AUG-1997;

XX: PR: 14-AUG-1997;

XX: PR: 14-AUG-1997;

XX: PR: 01-OCT-1997;

XX: PR: 97US-00724643.

XX: PR: 97US-0084419.

XX: PR: 97US-00846017.

XX: PR: 97US-00851843.

XX: PR: 97US-00854050.

XX: PR: 97US-00911312.

XX: PR: 97US-00912951.

XX: PR: 97US-00915503.

XX: PA: (GERO-) GERON CORP.

XX: PA: (UYTE-) UNIV TECHNOLOGY CORP.

XX: PI: Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;

XX: PI: Andrews WH;

XX: DR: WPI; 1998-171633/16.

XX: DR: N-PSDB; AAV2319.

XX: PT: Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.

XX: Claim 3; Fig 17; 387pp; English.

XX: The present sequence represents human telomerase reverse transcriptase (hTRT), which is a ribonucleoprotein. The present invention also describes the following methods: (A) determining whether a test compound

CC is a modulator of hTRT, by detecting the change in hTRT recombinant  
 CC protein or polynucleotide, on administration of the compound; (B)  
 CC preparation of recombinant telomerase by contacting a protein preparation  
 CC of hTRT with telomerase RNA component; (C) detection of the hTRT RNA or  
 CC protein in a sample by binding a relevant probe to the sample and  
 CC detecting the complex formed or in the case of RNA detection, amplifying  
 CC the product and correlating the presence of complex or amplification  
 CC product with presence of hTRT in the sample, and (D) increasing the  
 CC proliferation of a vertebrate cell by increasing hTRT expression; and (E)  
 CC the use of an agent that causes an increase in cell vertebrate cell.  
 CC proliferation to create a medicament that inhibits ageing. A protein  
 CC preparation of hTRT and the Polynucleotide encoding hTRT can be used in  
 CC the manufacture of medicaments for inhibiting the effect of ageing or  
 CC cancer. Inhibitors of telomerase can be used to treat conditions  
 CC that are associated with high telomerase activity. A protein preparation  
 CC of hTRT can also be used in the new methods  
 XX SQ Sequence 1132 AA:

QY	1	MPRAPCRAYRSLLRSHREVLPLATEVRLGPQGWRVLRQGDPAAFRALVAQCLVCPW	60	QY	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
DB	1	MPRAPCRAYRSLLRSHREVLPLATEVRLGPQGWRVLRQGDPAAFRALVAQCLVCPW	60	DB	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
QY	61	DARPPAAPSFRQSVCLKELVAVRLQRCERGAKNVLAFGALLDGARGGPPAFTTSVR	120	QY	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
DB	61	DARPPAAPSFRQSVCLKELVAVRLQRCERGAKNVLAFGALLDGARGGPPAFTTSVR	120	DB	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
QY	121	SYLPNTTDALRGCAWGLLRLRVDDVHLALARCAFLPVLYAPSACAVQVGPPLYQIGA	180	QY	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
DB	121	SYLPNTTDALRGCAWGLLRLRVDDVHLALARCAFLPVLYAPSACAVQVGPPLYQIGA	180	DB	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
QY	181	ATQARPPIPHASGPRRRLGCEBRAMHNSVRAGVPLGLPAGARRGGASRSPLPKRPR	240	QY	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
DB	181	ATQARPPIPHASGPRRRLGCEBRAMHNSVRAGVPLGLPAGARRGGASRSPLPKRPR	240	DB	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
QY	241	GAAPERIPVGQCSWAHQGRTRGPSPDRFCVYSPARAEATSLLEGALSGTPRHSHPSVG	300	QY	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
DB	241	GAAPERIPVGQCSWAHQGRTRGPSPDRFCVYSPARAEATSLLEGALSGTPRHSHPSVG	300	DB	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
QY	301	ROHHAGPSTSRPRPMDPCPPYTAETGHFLYSSGDKBQLRSFLLSLRPSLTGARL	360	QY	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
DB	301	ROHHAGPSTSRPRPMDPCPPYTAETGHFLYSSGDKBQLRSFLLSLRPSLTGARL	360	DB	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
QY	361	VETIFLGSRPWMPGTPLRPLPORYWNRPLFELLGNAQCYPYGVLLKTHCPLRAVT	420	QY	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
DB	361	VETIFLGSRPWMPGTPLRPLPORYWNRPLFELLGNAQCYPYGVLLKTHCPLRAVT	420	DB	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
QY	421	PAAGYCAREPQGSVAAPBEEEDTPRVLQVLLQHSSPQYTCFVACRLRYPPGIWGS	480	QY	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
DB	421	PAAGYCAREPQGSVAAPBEEEDTPRVLQVLLQHSSPQYTCFVACRLRYPPGIWGS	480	DB	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
QY	481	RHNERRFELNTKKRISIGKHAKLSQLETLWKMSYRDCAWLRRSPGVGCPAAEHLREI	540	QY	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
DB	481	RHNERRFELNTKKRISIGKHAKLSQLETLWKMSYRDCAWLRRSPGVGCPAAEHLREI	540	DB	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
QY	541	LAKELHWLMSVVVVELLSFFYYTTTFCNRPFYRKSVWSLQSIGIRQHLKRVQRE	600	QY	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
DB	541	LAKELHWLMSVVVVELLSFFYYTTTFCNRPFYRKSVWSLQSIGIRQHLKRVQRE	600	DB	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
QY	601	LSEAEVRQIREARPALLTERLRFPKPDLRPLPTNMDVGARTFRERKRAEFLTSRK	660	QY	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
DB	601	LSEAEVRQIREARPALLTERLRFPKPDLRPLPTNMDVGARTFRERKRAEFLTSRK	660	DB	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
QY	661	LFSVLYNERYARRPGSILGASVGLDDIHRAWRTEFLYRVAQDPPPELYPKVDTGATI	720	QY	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
DB	661	LFSVLYNERYARRPGSILGASVGLDDIHRAWRTEFLYRVAQDPPPELYPKVDTGATI	720	DB	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132
QY	721	PQDLTEVIASI1KPQNTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDQPYMRQFYAH	780	QY	1081	KLTRHRVTVYPLIGSLRTAQTLQRKLGTLTLEAAANPALSDFKTLID 1132

## RESULT 2

AAW90251

ID AAW90251 standard; protein; 1132 AA.

XX AAW90251;

XX DT 24-MAY-1999 (first entry)

XX DE Human catalytic telomerase sub-unit protein.

XX KW modulator; treatment; inhibit; cellular disorder; death; defect; cancer;

KW ageing; antisense; neoplastic cell; telomerase-related condition;

XX tumour cell.

OS Homo sapiens.

XX PN WO959040-A2.

XX PD 30-DEC-1998.

XX PF 09-JUN-1998; 98WO-EP003468.

XX PR 20-JUN-1997; 97DE-01026329.

XX PR 26-MAR-1998; 98DE-0101374.

XX PR 14-APR-1998; 98DE-01016496.

XX PA (PARB ) BAYER AG.

XX Hagen G, Siegmund H, Weichel W, Wick M, Zubov D;

XX DR WPI; 1999-081276/07.

XX DR N-PSDB; AAV72117.

XX PT New catalytically active subunit of human telomerase - used in the modulation of telomerase activity, particularly for treating cancer and ageing.

XX PS Claim 2; Fig 2; 76pp; German.

CC This sequence represents a novel human catalytic telomerase sub-unit (hTC). This protein can be used in screening assays to identify modulators of telomerase and to treat or inhibit cellular disorders, death, defects and/or other pathological processes involving telomerase, particularly cancer and ageing (also suitable for this are agents that stimulate, inhibit or mimic the activity of the subunit). Antisense

nucleic acids inhibit telomerase action (by binding to specific mRNA), particularly in neoplastic cells and may be expressed *in vivo*. Antibodies and fragments of the protein, used as probes or primers, are used to diagnose telomerase-related conditions (especially neoplasia) by (i) detecting abnormal levels of the subunit protein in body fluids or tissues or (ii) by measuring the amount of the encoding nucleic acid. Expression of the nucleic acid encoding the subunit mRNA is confined to tumour cells, in contrast to the ubiquitous expression of the telomerase

CC	therapeutic agents, for inhibition of telomerase expression and activity		
SQ	Sequence 1132 AA;		
Query Match	100.0%; Score 5861; DB 2; Length 1132;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 1132; Conservative 0; Mismatches 0; Gaps 0;			
QY	1 MPRAPCRAYRSLLRSHREVLPLATFVRRLGPQGWRVLRQGDPAFAFLVALVAOCLVCYFW 60		
DB	1 MPRAPCRAYRSLLRSHREVLPLATFVRRLGPQGWRVLRQGDPAFAFLVALVAOCLVCYFW 60		
QY	61 DARPPPAAPSFROYSCLEKELVARYLQLCERGAKNVLAFLDARGGGPPEAFTTSYR 120		RESULT 4
DB	61 DARPPPAAPSFROYSCLEKELVARYLQLCERGAKNVLAFLDARGGGPPEAFTTSYR 120		AAY32090 standard; protein: 1132 AA.
QY	121 SYLPNTVDALRGSSAWGLLRLRRVGDDVHLARCALFVLVAPSACAVQCGPPLYQJGA 180		ID AAY32090
DB	121 SYLPNTVDALRGSSAWGLLRLRRVGDDVHLARCALFVLVAPSACAVQCGPPLYQJGA 180		XX
QY	181 ATQARPPPHASGPERRRLGCERBAAWHSVREAGVPLGLPAGARRGGSARSLSLPLPKRPR 240		AAW32090;
DB	181 ATQARPPPHASGPERRRLGCERBAAWHSVREAGVPLGLPAGARRGGSARSLSLPLPKRPR 240		XX
QY	241 GAAPPERTSYVGCGSWAHPGTRGFSDRGFCVWSPARAEEATLEGALSGTGHSHPSYG 300		DT 17-JAN-2000 (first entry)
DB	241 GAAPPERTSYVGCGSWAHPGTRGFSDRGFCVWSPARAEEATLEGALSGTGHSHPSYG 300		XX
QY	301 ROHHAGPSTSRPRPWDTPCPPYYAETKHFYLSSGDKBOLRSPFLSSLRPSLTGARL 360		Human telomerase reverse transcriptase (hTERT).
DB	301 ROHHAGPSTSRPRPWDTPCPPYYAETKHFYLSSGDKBOLRSPFLSSLRPSLTGARL 360		DE
QY	361 VETIFLGSRWMPGTPRPLPRLPORYWQNRPLFELLGNAHQCPYGVNLKTHCPLRAVT 420		XX
DB	361 VETIFLGSRWMPGTPRPLPRLPORYWQNRPLFELLGNAHQCPYGVNLKTHCPLRAVT 420		DE Human telomerase reverse transcriptase; human; hTERT; cell proliferation; cancer.
QY	421 PAAGVYCAREKRPQGSVAAPEEEEDTDPRRLVYOLLROHSSPNQVYGFYRACLARRLYPPGIGWS 480		XX
DB	421 PAAGVYCAREKRPQGSVAAPEEEEDTDPRRLVYOLLROHSSPNQVYGFYRACLARRLYPPGIGWS 480		KW
QY	481 RHNERFLNKTKEFISLGKAHLSQLELTWKMSYRDCAWLRRSPFGVGYCPAAEHLREI 540		XX
DB	481 RHNERFLNKTKEFISLGKAHLSQLELTWKMSYRDCAWLRRSPFGVGYCPAAEHLREI 540		OS Homo sapiens.
QY	541 LAKFDHWLMSVVYVLLRSFYYTTFFQKRNLFYRKSWSKLQSIGTRQHILKRVQRE 600		XX
DB	541 LAKFDHWLMSVVYVLLRSFYYTTFFQKRNLFYRKSWSKLQSIGTRQHILKRVQRE 600		PN WO950386-A2.
QY	601 LSEAEVROHREARPALLTSRLRFKPKDGRARPTNMMDYVGARTFRREKRAEELTSYKA 660		XX
DB	601 LSEAEVROHREARPALLTSRLRFKPKDGRARPTNMMDYVGARTFRREKRAEELTSYKA 660		PD 07-OCT-1999.
QY	661 LFSVLYNERARRPGHLGASVGLDDIHARWFYVLRQDPPELYFKYDVTGAYDTI 720		XX
DB	661 LFSVLYNERARRPGHLGASVGLDDIHARWFYVLRQDPPELYFKYDVTGAYTI 720		PP 31-MAR-1999;
QY	721 PQDRITEVIAASIKPQNTYCVRRYAVQXAAHGFYRKAFKSHYSTLTDLQPYMRQFYAHL 780		XX
DB	721 PQDRITEVIAASIKPQNTYCVRRYAVQXAAHGFYRKAFKSHYSTLTDLQPYMRQFYAHL 780		PR 31-MAR-1998;
QY	781 QETSPLRDAVVIQEQQSLNEAASSGLFDYFLRFMCHAVIRGKSYVOCOGIPQGSTLSTL 840		PR 03-AUG-1998;
DB	781 QETSPLRDAVVIQEQQSLNEAASSGLFDYFLRFMCHAVIRGKSYVOCOGIPQGSTLSTL 840		XX
QY	841 LCSLCYGMENKLFAGIRDGLLRLVDDFLVTPHFLTHAKTFPLRTLYGVPYEGCVNL 900		(GERO-) GERON CORP.
DB	841 LCSLCYGMENKLFAGIRDGLLRLVDDFLVTPHFLTHAKTFPLRTLYGVPYEGCVNL 900		PA
QY	901 RKTIVNFVPEDEALGGTAVQMPAHGLFWMCGLLIDFLVTPHFLTHAKTFPLRTLYGVPYEGCVNL 960		PI Marin GB;
DB	901 RKTIVNFVPEDEALGGTAVQMPAHGLFWMCGLLIDFLVTPHFLTHAKTFPLRTLYGVPYEGCVNL 960		XX
QY	961 NRGPXAGRMRRKLFGVRLKCHSLSFLDQVNLSQTVCNTYKILLQDAYRPHACVLQLP 1020		WP: 1999-610842/52.
			DR N-PSDB; AAZ20279.
			XX
			PT New catalytic polypeptide and polynucleotide, useful for increasing catalytic activity in a cell.
			XX
			Claim 13; Fig 1; 24pp; English.
			CC The present sequence represents human telomerase reverse transcriptase (hTERT). Human telomerase is a target for diagnosing and treating diseases relating to cell proliferation and senescence, such as cancer, or for increasing the proliferative capacity of a cell. A claimed method for recombinant hTERT polynucleotide encoding an hTERT variant in which residues 192-323, 200-323, 192-271, 222-240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 of the present sequence are deleted.
			CC A claimed method of preparing recombinant telomerase involves contacting a recombinant hTERT deletion mutant (as above) with a telomerase RNA component such that the 2 proteins associate to form a complex capable of catalysing the addition of nucleotides to a telomerase substrate. A claimed method for reducing telomerase activity in a cell involves introducing a recombinant polynucleotide encoding an hTERT variant having a deletion of amino acids 192-450, 560-565, 637-660, 638-660, 748-764 or 1055-1071 of the present sequence
			XX
			SQ Sequence 1132 AA;
			Query Match 100.0%; Score 5961;
			Best Local Similarity 100.0%; Pred. No. 0;
			Mismatches 0; Indels 0; Gaps 0;
			QY 1 MPRAPCRAYRSLLRSHREVLPLATEVRLGPQGWRVLRQGDPAAFRALVAQCLVCYFW 90

Db	1 MPRAPCRAVRSLLSHREVLPLATEFVRRGPQWRLVQGDPAFAFLAYAQCLVCVPW 60	Db	1081 KLTHRHVTYVPLIGSLRATQTLRKLPGTITLAEAAANPALPSDFKTYLD 1132
Qy	61 DARPPAAPSQRVSCLKELVARVLORLCEGAKNVLAFGFLALDARGGGPPEAFTTSVR 120	Qy	RESULT 5 AY43621 ID AA43621 standard; protein; 1132 AA.
Db	61 DARPPAAPSQRVSCLKELVARVLORLCEGAKNVLAFGFLALDARGGGPPEAFTTSVR 120	Db	XX
Qy	121 SYLPNTVTDALRGSGAWGLLARRGYDDVLHILLARCAFLVAPSCAYQVGCPPLYOLGA 180	Qy	AC
Db	121 SYLPNTVTDALRGSGAWGLLARRGYDDVLHILLARCAFLVAPSCAYQVGCPPLYOLGA 180	Db	XX
Qy	121 ATQARPPPHASGPRRLGCERAWNNTSVEAGVPLGLPAGARRGCSAARSPLPKRPR 240	Qy	DT 26-JAN-2000 (first entry)
Db	121 ATQARPPPHASGPRRLGCERAWNNTSVEAGVPLGLPAGARRGCSAARSPLPKRPR 240	Db	XX
Qy	181 GAAPEPERTPVQGSWAHPGPTRGPDGFCVSPARAAEATSLEGALSGTRSHAPSVG 300	Qy	A human telomerase reverse transcriptase (TRT) polypeptide.
Db	181 GAAPEPERTPVQGSWAHPGPTRGPDGFCVSPARAAEATSLEGALSGTRSHAPSVG 300	Db	XX
Qy	241 RQHHAGPPSTSRRPPWDTPCPVVAETKHFLYSSCDKEOLRPSFLISURPSLTGARL 360	Qy	Human; telomerase reverse transcriptase; TRT; T lymphocyte activation; dendritic cell; telomerase activity; cancer cell; proliferating cell; immunological; destruction; telomerase; telomerase; proliferation disease.
Db	241 RQHHAGPPSTSRRPPWDTPCPVVAETKHFLYSSCDKEOLRPSFLISURPSLTGARL 360	Db	XX
Qy	241 RQHHAGPPSTSRRPPWDTPCPVVAETKHFLYSSCDKEOLRPSFLISURPSLTGARL 360	Qy	XX
Db	301 VETIFLGSRPPMPGCPPRRLPBLPQRYWQMRPLFELIGNTAQCPYGLKTHCPIBRAAT 420	Db	XX
Qy	301 VETIFLGSRPPMPGCPPRRLPBLPQRYWQMRPLFELIGNTAQCPYGLKTHCPIBRAAT 420	Qy	9 WO-US006898.
Db	301 VETIFLGSRPPMPGCPPRRLPBLPQRYWQMRPLFELIGNTAQCPYGLKTHCPIBRAAT 420	Db	PN WO950392-A1.
Qy	361 PAAGYCAREPQGSVAAPEEEDDPDRRLVQLRQHSSPQWVYGFVACRLRLLVPPGJWGS 480	Qy	XX
Db	361 PAAGYCAREPQGSVAAPEEEDDPDRRLVQLRQHSSPQWVYGFVACRLRLLVPPGJWGS 480	Db	PD 07-OCT-1999.
Qy	421 PAAAGCAREPQGSVAAPEEEDDPDRRLVQLRQHSSPQWVYGFVACRLRLLVPPGJWGS 480	Qy	XX
Db	421 PAAAGCAREPQGSVAAPEEEDDPDRRLVQLRQHSSPQWVYGFVACRLRLLVPPGJWGS 480	Db	PF 30-MAR-1999;
Qy	481 RHNERFLRFLRTKCFKLSGKHAKLSSLQBLTWRMSVRDCAWLRRSPGTVQYTFVACRLRLLVPPGJWGS 540	Qy	XX
Db	481 RHNERFLRFLRTKCFKLSGKHAKLSSLQBLTWRMSVRDCAWLRRSPGTVQYTFVACRLRLLVPPGJWGS 540	Db	PR 31-MAR-1998;
Qy	541 LAKFLHMLMSVYNTLLRSPPXYTTTFOQRLFPRKSWSKLQIGRQLKRVQLE 600	Qy	XX
Db	541 LAKFLHMLMSVYNTLLRSPPXYTTTFOQRLFPRKSWSKLQIGRQLKRVQLE 600	Db	PA (GERO-) GERON CORP.
Qy	601 LSEAEVROQEARPAULTSRDRFPIKPGDGLRPVIVNDYVQARTPFRKERAERLTSRVA 660	Qy	XX
Db	601 LSEAEVROQEARPAULTSRDRFPIKPGDGLRPVIVNDYVQARTPFRKERAERLTSRVA 660	Db	XX
Qy	601 LSEAEVROQEARPAULTSRDRFPIKPGDGLRPVIVNDYVQARTPFRKERAERLTSRVA 660	Qy	Eliciting an in vivo immune response for prevention and treatment of cancers.
Db	601 LSEAEVROQEARPAULTSRDRFPIKPGDGLRPVIVNDYVQARTPFRKERAERLTSRVA 660	Db	XX
Qy	661 LFSVINYERARRPGLLGASVYLGLDDIHRARWTFVLRVAODPPPELFVYDVTGAYDTI 720	Qy	Claim 3; Fig 1; 26pp; English.
Db	661 LFSVINYERARRPGLLGASVYLGLDDIHRARWTFVLRVAODPPPELFVYDVTGAYDTI 720	Db	XX
Qy	661 LFSVINYERARRPGLLGASVYLGLDDIHRARWTFVLRVAODPPPELFVYDVTGAYDTI 720	Qy	The present sequence represents a human telomerase reverse transcriptase (TRT) polypeptide. The protein is used in the method of the invention.
Db	721 PQDRTEVATISIlikONTYCYTRAYVQKAAGHTRKAPEKSHVSLTLDQYMDQVTAHL 780	Db	CC The specific sequence describes a method for activating a T lymphocyte, comprising contacting the T lymphocyte with a dendritic cell that expresses a TRT peptide in the context of a MHC class I or MHC class II molecule. The protein causes induction of an in vivo immunological response to telomerase activity. Cancer cells are characterized by expression of endogenous TRT gene and the presence of detectable telomerase activity. Therefore, by eliciting a specific immune response to TRT or to TRT-expressing cells, it is possible to selectively target proliferating cells for immunological destruction. The method is used to elicit an in vivo immune response to telomerase by activating a T lymphocyte, and is useful for prevention and treatment of cancers and other proliferation diseases/conditions
Qy	721 PQDRTEVATISIlikONTYCYTRAYVQKAAGHTRKAPEKSHVSLTLDQYMDQVTAHL 780	Qy	XX
Db	781 QETSPRLDIAVVIQSSSLNEASGLEDFVLFRMCHHAIRGKSYVQCGPOGSILSTL 840	Db	CC
Qy	781 QETSPRLDIAVVIQSSSLNEASGLEDFVLFRMCHHAIRGKSYVQCGPOGSILSTL 840	Qy	CC
Db	841 LCSLCYGMENKLFLAGIRDCCLLRLVDFLLVTPHTKACTFLTRLVRGPEYGVNL 900	Db	CC
Qy	841 LCSLCYGMENKLFLAGIRDCCLLRLVDFLLVTPHTKACTFLTRLVRGPEYGVNL 900	Qy	CC
Db	901 RKTUVNPVEDAEGTAFQMPAHLFPWMCILLDTRLEVQSDYSSYARTSIRASLT 960	Db	CC
Qy	901 RKTUVNPVEDAEGTAFQMPAHLFPWMCILLDTRLEVQSDYSSYARTSIRASLT 960	Qy	1 MPAPRPRCAVRSLRSHREVLPLATFVRLGPQSWRLVQGDPAFAFLVALVQCLVCVPW 60
Db	901 RKTUVNPVEDAEGTAFQMPAHLFPWMCILLDTRLEVQSDYSSYARTSIRASLT 960	Db	1 MPAPRPRCAVRSLRSHREVLPLATFVRLGPQSWRLVQGDPAFAFLVALVQCLVCVPW 60
Qy	961 NRGKAGGRNRRKLGFLVRLKUCHSLFDLQVNSLQVTCNTYKILLQATRFHACVTLQLP 1020	Qy	61 DARPAPPAAFSFQVSCLELVALVQRLICERGAKNVLAFGFALDGARGGPPEAFTTSVR 12
Db	961 NRGKAGGRNRRKLGFLVRLKUCHSLFDLQVNSLQVTCNTYKILLQATRFHACVTLQLP 1020	Db	61 DARPAPPAAFSFQVSCLELVALVQRLICERGAKNVLAFGFALDGARGGPPEAFTTSVR 12
Qy	1021 FHQOWKNPTFFLRVTSIDTASLCYSLIKAGNMSLGAKGAGGLPSEAYOWLCHOAFLL 1080	Qy	121 SYLPNTVTDALRSGWGLLRRYDVLVHLLRCALFVLYVLSVCAYQVCGPPLYOLGA 18
Db	1021 FHQOWKNPTFFLRVTSIDTASLCYSLIKAGNMSLGAKGAGGLPSEAYOWLCHOAFLL 1080	Db	121 SYLPNTVTDALRSGWGLLRRYDVLVHLLRCALFVLYVLSVCAYQVCGPPLYOLGA 18
Qy	1081 KLTHRHVTYVPLLSLRTAATQLSKLPGTITLAEAAANPALPSDFKTYLD 1132	Qy	121 SYLPNTVTDALRSGWGLLRRYDVLVHLLRCALFVLYVLSVCAYQVCGPPLYOLGA 18
Db	1081 KLTHRHVTYVPLLSLRTAATQLSKLPGTITLAEAAANPALPSDFKTYLD 1132	Db	161 ATQARPPPHASGPRRLGCERAWNNTSVEAGVPLGLPAPGARRGGSASRSLPPLPKRPR 161



Db	421	PAAGVCREREKFGSVAPEEEDTPRRLVQLLQHSSPWQYGFVRACLRLVPPGLWGS	480	XX Umeyama A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
Qy	481	RHNERERFLRNTYKKFISLGKHAKLSQLBLTWSMVRSCAWIIRRSPGCVCPAAEHRLREB1	540	PI PI XX WPI ; 2001-425556 / 45 .
Db	481	RHNERERFLRNTYKKFISLGKHAKLSQLBLTWSMVRSCAWIIRRSPGCVCPAAEHRLREB1	540	DR N-PSDB ; AAH48235 .
Qy	541	LAKELHWMSTYVVEILRSFFYVTTETFOKNRLFFYKTSWSKLSLOGIGRQLKRVQLE	600	XX Cells capable of differentiating into cardiomyocytes and originating in bone marrow or umbilical blood cells for study of cardiomyocyte
Db	541	LAKELHWMSTYVVEILRSFFYVTTETFOKNRLFFYKTSWSKLSLOGIGRQLKRVQLE	600	PT PT XX differentiation and treatment of heart disease.
Qy	601	LSEAEVTRQHREARPALTSURFIPKPKDGRPIVNNDDYVVGARTPRREKAERLTSRVKA	660	PS Claim 87; Page 143-147; 183pp; Japanese .
Db	601	LSEAEVTRQHREARPALTSURFIPKPKDGRPIVNNDDYVVGARTPRREKAERLTSRVKA	660	XX The present invention provides cells originating in the human bone marrow or umbilical blood cells which are capable of differentiating into cardiomyocytes. These cells are useful in the treatment of diseases involving heart muscle degeneration, such as myocardial infarction, and the study of cardiomyocyte differentiation. The present sequence is a CC protein described in the exemplification of the invention
Qy	661	LFSVNLNEYERARRPGLIGASVIGLDDIHRANTFVLRVRAODPPPELYFVKVDVGTAYDT1	720	XX Sequence 1132 AA;
Db	661	LFSVNLNEYERARRPGLIGASVIGLDDIHRANTFVLRVRAODPPPELYFVKVDVGTAYDT1	720	Query Match 100.0% ; Score 5961 ; DB 4 ; Length 1132 ; Best Local Similarity 100.0% ; Pred. No 0 ; Matches 1132 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
Qy	721	PQRDLTEVIASIPIKPOINTCYCVRAYAVYQKAAGHGVKAFKSHVSLTLIDQPYMQFQVAHL	780	Qy 1 MPRAPRCRAVSLRSLSHREYREVLPATFVERLGPQSWRLVQGDPAFAFLVAVQCLVCPW 60
Db	721	PQRDLTEVIASIPIKPOINTCYCVRAYAVYQKAAGHGVKAFKSHVSLTLIDQPYMQFQVAHL	780	Db 1 MPRAPRCRAVSLRSLSHREYREVLPATFVERLGPQSWRLVQGDPAFAFLVAVQCLVCPW 60
Qy	781	QETSPRDVAVIEQSSSLNEASSGLPFDVFRFMCHAVRERGKSIVQCGIPQSISLSTL	840	Qy 61 DARRPPAAPSFRQVSCLKELVARYLQRLCERGAKVLAFCALDFARGGPPEAFTTSVR 120
Db	781	QETSPRDVAVIEQSSSLNEASSGLPFDVFRFMCHAVRERGKSIVQCGIPQSISLSTL	840	Db 61 DARRPPAAPSFRQVSCLKELVARYLQRLCERGAKVLAFCALDFARGGPPEAFTTSVR 120
Qy	841	LCSLCYGDMEKLFAAGRDRGILLRVDDELLVTPH1THATKFLTLLVRCVPEYGCVNVL	900	Qy 61 DARRPPAAPSFRQVSCLKELVARYLQRLCERGAKVLAFCALDFARGGPPEAFTTSVR 120
Db	841	LCSLCYGDMEKLFAAGRDRGILLRVDDELLVTPH1THATKFLTLLVRCVPEYGCVNVL	900	Db 61 DARRPPAAPSFRQVSCLKELVARYLQRLCERGAKVLAFCALDFARGGPPEAFTTSVR 120
Qy	901	RKTIVVNFPVEDBALGTAFYQMPAHGCLFPNGCGLLDTDTTLEVQSDYSYARTSISTRASLT	960	Qy 121 SYLNPNTVTDALRGSGAWGHLIRRYGDPDVYLHLLARCALFVTLVADPSCAYQVCGPPLYQLGA 180
Db	901	RKTIVVNFPVEDBALGTAFYQMPAHGCLFPNGCGLLDTDTTLEVQSDYSYARTSISTRASLT	960	Db 121 SYLNPNTVTDALRGSGAWGHLIRRYGDPDVYLHLLARCALFVTLVADPSCAYQVCGPPLYQLGA 180
Qy	961	NRGFKAGRMRKLFGVLRKCHSLFDLQVNSLOTCTNIYKILLQAYRFHACVLQLP	1020	Qy 181 ATQARPPPHASGPRRLGCERAWNHVSREAGVPGUGLPAFARRGGSAASRLSPPKRPRR 240
Db	961	NRGFKAGRMRKLFGVLRKCHSLFDLQVNSLOTCTNIYKILLQAYRFHACVLQLP	1020	Db 181 ATQARPPPHASGPRRLGCERAWNHVSREAGVPGUGLPAFARRGGSAASRLSPPKRPRR 240
Qy	1021	FHQOQWKNPTEFLRVTISDTASLCYSLIKAKNAGMISLGKAGAAGPUSPEAVQWLQHQAFL	1080	Qy 241 GAAPEPERTVPGOGGSWAHPGRTGFDRCFVIVSPARPAEETLEGALSCTRISHPSVVG 300
Db	1021	FHQOQWKNPTEFLRVTISDTASLCYSLIKAKNAGMISLGKAGAAGPUSPEAVQWLQHQAFL	1080	Db 241 GAAPEPERTVPGOGGSWAHPGRTGFDRCFVIVSPARPAEETLEGALSCTRISHPSVVG 300
Qy	1081	KLTRHRVTVYPLGLSISRTAQTLSRKLPGTTLTALFAANPALPSDFKTYLD	1132	Db 301 RQHAGGPSTSRRPRWDTPCPPTYAETKHFLLSGDKBQLRPSFLSSLRPSLTGARRL 360
Db	1081	KLTRHRVTVYPLGLSISRTAQTLSRKLPGTTLTALFAANPALPSDFKTYLD	1132	Db 301 RQHAGGPSTSRRPRWDTPCPPTYAETKHFLLSGDKBQLRPSFLSSLRPSLTGARRL 360
RESULT 7				Db 361 VETFLGSRPWPMPPTPRLPRLPORYWQMPRLPFLLELLGHQAQCYPGVLLKTHCPLRAAVT 420
AAG64859	ID	AAG64859 standard; protein; 1132 AA.		Db 361 VETFLGSRPWPMPPTPRLPRLPORYWQMPRLPFLLELLGHQAQCYPGVLLKTHCPLRAAVT 420
AC				Qy 421 PAAGYCAREKPOGGSVAAPPEDDTDPRRLVQLLROHSSPWHQVYGFVACRLRVPGLWGS 480
XX				Db 421 PAAGYCAREKPOGGSVAAPPEDDTDPRRLVQLLROHSSPWHQVYGFVACRLRVPGLWGS 480
DT	21-SEP-2001	(first entry)		Db 421 PAAGYCAREKPOGGSVAAPPEDDTDPRRLVQLLROHSSPWHQVYGFVACRLRVPGLWGS 480
XX				Db 481 RHNRERERFLNTKKPISLGKHAKLSQLQETWKSMDVCAWLRSSGVGCPAAEHRLREEI 540
DE		Heart muscle cell differentiation related protein SEQ ID NO : 31 .		Db 481 RHNRERERFLNTKKPISLGKHAKLSQLQETWKSMDVCAWLRSSGVGCPAAEHRLREEI 540
XX		Heart muscle cell; human; cell differentiation; heart disease.		Qy 541 LAKELHWMSTYVVEILRSFFYVETTETTFOXNLRFPEYRKSVWKSQSIGRHLLRQVLR 600
OS		Homo sapiens.		Db 541 LAKELHWMSTYVVEILRSFFYVETTETTFOXNLRFPEYRKSVWKSQSIGRHLLRQVLR 600
XX				Qy 601 LSEAEVROREARPALLTSRLRF1PKPDGLRPTWMDYYVGAFTREKEKAEIITSRVKA 660
PN	WO200148151-A1.			Db 601 LSEAEVROREARPALLTSRLRF1PKPDGLRPTWMDYYVGAFTREKEKAEIITSRVKA 660
XX				Db 661 LFSVNLNEYERARRPGLIGASVGLDDIHRARWRTFVLRVRAODPPPELYFVKVDVGTAYDT1 720
PD	05-JUL-2001 .			Db 661 LFSVNLNEYERARRPGLIGASVGLDDIHRARWRTFVLRVRAODPPPELYFVKVDVGTAYDT1 720
XX				PA (KYOW ) KYOWA HAKKO KOGYO KK .

Qy 721 PQRRLTEVIASTIKPQNTYCVRRAYVYOKAAIGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780  
 Db 721 PQRRLTEVIASTIKPQNTYCVRRAYVYOKAAIGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780  
 Qy 781 QETSPRLDAVIEQSSENEASSGGLFDYVLFREMCHAVRTRGKSYVQCGIPQGSILSTL 840  
 Db 781 QETSPRLDAVIEQSSENEASSGGLFDYVLFREMCHAVRTRGKSYVQCGIPQGSILSTL 840  
 Qy 841 LCSLCYGDMENTKLFAIGRRDGILLRVDDEFLVTPHILTHAKTFLRLVGRVPEYCCVNL 900  
 Db 841 LCSLCYGDMENTKLFAIGRRDGILLRVDDEFLVTPHILTHAKTFLRLVGRVPEYCCVNL 900  
 Qy 901 RKFVNPNEVEDALGGTAFVQMPAHGLFPWCGLLIDRTLEVSQDSYSTARTSIRASLT 960  
 Db 901 RKTIVNPNEVEDALGGTAFVQMPAHGLFPWCGLLIDRTLEVSQDSYSTARTSIRASLT 960  
 Qy 961 NRGFKAQRNMRKLFGTQLRKCHSLFLDLQVNSLQTVCTNYKILLQAYRFHACVLQUP 1020  
 Db 961 NRGFKAQRNMRKLFGTQLRKCHSLFLDLQVNSLQTVCTNYKILLQAYRFHACVLQUP 1020  
 Qy 1021 FHQQVWNKPTEFLRVISDTASLYCSTIKAKNAGMSLGAKAAGLPSAEVQLCHQATFL 1080  
 Db 1021 FHQQVWNKPTEFLRVISDTASLYCSTIKAKNAGMSLGAKAAGLPSAEVQLCHQATFL 1080  
 Qy 1081 KLTRHRVTTYDPLGLSURTAQTQLSRKLPGTITLAEAANPALPSDFKTILD 1132  
 Db 1081 KLTRHRVTTYDPLGLSURTAQTQLSRKLPGTITLAEAANPALPSDFKTILD 1132

	Query	Match	Score	Length
	Qy	100.0% ; Score 5961;	5961	DB 4 ; Length 1132;
	Db	Best Local Similarity 100.0% ; Pred. No. 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ; Matches 1132; Conservative 0;		
	Qy	1 MPRAPRCRAVRSLLSRSHREVLPLATFYRRLGPQGWRLVQRGDPAAFRALVAOCLVCPW 60	1	
	Db	1 MPRAPRCRAVRSLLSRSHREVLPLATFYRRLGPQGWRLVQRGDPAAFRALVAOCLVCPW 60	1	
	Qy	61 DARPPAAPSFRQSCILKELVARVLRQLCERGAKNVLAEGFALLDGARGGPPPEFTTSVR 120	61	
	Db	61 DARPPAAPSFRQSCILKELVARVLRQLCERGAKNVLAEGFALLDGARGGPPPEFTTSVR 120	61	
	Qy	121 SYLPLNTUDALRSGAWGILLRNGDDYLVHLARCALFPLVAPSCAYQVCGPLPLYQGQA 180	121	
	Db	121 SYLPLNTUDALRSGAWGILLRNGDDYLVHLARCALFPLVAPSCAYQVCGPLPLYQGQA 180	121	
	Qy	181 ATQRPPPHASGRRLGCERAWNHSYREAGVPLGLPAGPARRGGSASRSLPLPKRPRR 240	181	
	Db	181 ATQRPPPHASGRRLGCERAWNHSYREAGVPLGLPAGPARRGGSASRSLPLPKRPRR 240	181	
	Qy	241 GAAPEPERTPVGGGSWAHPGRTRGSPDRGFCVSPARPAEATSLEGALSTGRHSHPSVG 300	241	
	Db	241 GAAPEPERTPVGGGSWAHPGRTRGSPDRGFCVSPARPAEATSLEGALSTGRHSHPSVG 300	241	
	Qy	301 RQHAGPSTSRRPRPNDTPCPVYAAETKHELYSSCDKEOLRPSFLSSLRPSLTGARRL 360	301	
	Db	301 RQHAGPSTSRRPRPNDTPCPVYAAETKHELYSSCDKEOLRPSFLSSLRPSLTGARRL 360	301	
	Qy	361 VETIFLGSRPNMPTPRLPRLPRLPQLPQMRPLPLELGNHQCPGVULLKTHCPPLRAVT 420	361	
	Db	361 VETIFLGSRPNMPTPRLPRLPRLPQLPQMRPLPLELGNHQCPGVULLKTHCPPLRAVT 420	361	
	Qy	421 PAGVCAREPKQGSAAPEEEEDTPDPLVQLLROHQHSSPQWQYGFVACLRLVPGLWGS 480	421	
	Db	421 PAGVCAREPKQGSAAPEEEEDTPDPLVQLLROHQHSSPQWQYGFVACLRLVPGLWGS 480	421	
	Qy	481 RHNERERFLRNTKFKISLGKHAKLSQLBLTWKSVRDCAWLRSPGTYCVPAAEHHLREEI 540	481	
	Db	481 RHNERERFLRNTKFKISLGKHAKLSQLBLTWKSVRDCAWLRSPGTYCVPAAEHHLREEI 540	481	
	Qy	541 LAKFLHMLSMYYVEILRSFFYVTTETFOKNRLPFYRKSWMSKLSIGIROHLKRVQLE 600	541	
	Db	541 LAKFLHMLSMYYVEILRSFFYVTTETFOKNRLPFYRKSWMSKLSIGIROHLKRVQLE 600	541	
	Qy	601 LSEAETQRHREARPALTSURFPIKPDGLRPIVMDYVVGARTFREKERAERLTSRVKA 660	601	
	Db	601 LSEAETQRHREARPALTSURFPIKPDGLRPIVMDYVVGARTFREKERAERLTSRVKA 660	601	
	Qy	661 LFSV1AYERARRPGLGASVGLDODIHRAWRTFVLRVRAODPPEFLYVVKDVTGAYDTI 720	661	
	Db	661 LFSV1AYERARRPGLGASVGLDODIHRAWRTFVLRVRAODPPEFLYVVKDVTGAYDTI 720	661	
	Qy	721 PQDRLTEVIASIKPONTYCVRRYAVOKAAGHYRKAFKSHVSTLTDQPYMRQFV AHL 780	721	
	Db	721 PQDRLTEVIASIKPONTYCVRRYAVOKAAGHYRKAFKSHVSTLTDQPYMRQFV AHL 780	721	
	Qy	781 QETSPRLDAVIEQSSSLNEASGGFLDVFVRMCFHVAVRFRGSVYQCGIPQGSILSTL 840	781	
	Db	781 QETSPRLDAVIEQSSSLNEASGGFLDVFVRMCFHVAVRFRGSVYQCGIPQGSILSTL 840	781	
	Qy	841 LCSLCYGDMENTKLFGIRRQGLLFLVDDFLVTHLTHAKTFLRLVRCVPECCVNL 900	841	
	Db	841 LCSLCYGDMENTKLFGIRRQGLLFLVDDFLVTHLTHAKTFLRLVRCVPECCVNL 900	841	
	Qy	901 RKTVNPNPVEDALEGSTAFQMPAHGLFPNGLJLIDTRTLEVSQDSSYARTSIRASLT 960	901	
	Db	901 RKTVNPNPVEDALEGSTAFQMPAHGLFPNGLJLIDTRTLEVSQDSSYARTSIRASLT 960	901	
	Qy	961 NRGFAGRNNMRKLCFLQVRLKCHSFLDQVNSLQTVCPNIYKILLQAYRFHACVLQUP 1020	961	
	Db	961 NRGFAGRNNMRKLCFLQVRLKCHSFLDQVNSLQTVCPNIYKILLQAYRFHACVLQUP 1020	961	

Sequence 1132 AA;

Human protein #2 .  
 XX Angiogenesis; cardiant; cell differentiating agent; bone marrow;  
 KW heart muscle cell; heart disease; human.  
 XX Homo sapiens.  
 PN WO200148149-A1.  
 XX PR 28-DEC-1999; 99JP-00372826.  
 XX PD 05-JUL-2001.  
 XX PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX PF 28-FEB-2000; 2000WO-JP001148.  
 XX DR WPI; 2001-418452/44.  
 DR N-PSDB; AAH49601.  
 XX New adult bone marrow-originated cells capable of differentiating into heart muscle cells, applicable as remedies for various heart diseases particularly with damaged heart muscle accompanying degeneration.  
 XX Disclosure; Page 128-134; 158pp; Japanese.  
 XX The present invention relates to cells isolated from bone marrow, which are capable of at least differentiating into heart muscle cells. The cells are applicable as remedies for various heart diseases particularly with damaged heart muscle accompanying degeneration. The present sequence was used to illustrate the present invention.  
 XX Sequence 1132 AA;

Qy 1021 FHQQWKNPTEFLRVISDTASLCYSTIKAKNAGMSIAGKGAAGPLPEAYOWLCHOAFL 1080  
 Db 1021 FHQQWKNPTEFLRVISDTASLCYSTIKAKNAGMSIAGKGAAGPLPEAYOWLCHOAFL 1080

Qy 1081 KLTTRHRYTYVPLGSIRTAQTLRSRKLPGTTLTALEAAANPALPSDFKTILD 1132  
 Db 1081 KLTTRHRYTYVPLGSIRTAQTLRSRKLPGTTLTALEAAANPALPSDFKTILD 1132

**RESULT 9**  
**AAB99330**  
**ID AAB99330 standard; protein; 1132 AA.**  
**XX**  
**AC AAB99330;**  
**XX**

DT 26-SEP-2001 (first entry)

XX Human telomerase protein sequence SEQ ID NO:31.

XX Differentiation; heart muscle cell; cytokine; transcription factor;  
 KW proliferation; surface antigen; heart disease; cardiomycocyte;  
 KW bone marrow; umbilical blood cell; heart muscle degeneration;  
 KW myocardial infarction.

XX OS Homo sapiens.

XX PN WO200148150-A1.

XX PD 05-JUL-2001.

XX PF 02-NOV-2000; 2000WO-JP0007741.

XX PR 28-DEC-1990; 99JP-00372826.

XX PR 28-FEB-2000; 2000WO-JP001148.

PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Umezawa, A., Hata, J., Fukuda, K., Ogawa, S., Sakurada, K., Gojo, S.;  
 Yamada, Y;

XX DR WPI; 2001-425655/45.  
 DR N-PSPDB; AAI44366.

PT Cells capable of differentiating into cardiomycocytes and originating in  
 bone marrow or umbilical blood cells for study of cardiomyocyte  
 differentiation and treatment of heart disease.

PS Claim 146; Page 137-141; 187pp; Japanese.

CC The present invention describes cells originating in bone marrow or  
 umbilical blood cells which are capable of differentiating into  
 cardiomyocytes. Also described are: (1) cardiomyocytes produced by the  
 differentiation of the cells; (2) a method for carrying out the  
 differentiation into cardiomyocytes, regulated by a promotional and/or  
 inhibitory factor; (3) a method for the differentiation of the cells into  
 cell types other than cardiomyocytes; (4) drug compositions promoting the  
 formation of heart muscle and regeneration of heart tissue which contain  
 the cells; (5) a method for the production of antibodies which recognise  
 the cells, especially antibodies which recognise a surface antigen on the  
 cells; (6) a method for screening factors which promote the proliferation  
 of the cells; (7) a method for immortalising the cells by expressing  
 telomerase in them; (8) drug compositions for the treatment of heart  
 disease which contain the immortalised cells; and (9) cell-line  
 supernatant from the culture of the cells and its use in promoting their  
 differentiation into cardiomyocytes. The cells are used in the treatment  
 of diseases involving heart muscle degeneration, such as myocardial  
 infarction and in the study of cardiomyocyte differentiation. AAI44351 to  
 AAB99335 and AAB99915 to AB99935 represent sequences used in the  
 specification of the present invention

XX Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 4; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPCRATSLRSLSHYREVLPATFVRLLPQEWRLYORGDPAPAFRALVAQCLVCVPW 60  
 Db 1 MPRAPCRATSLRSLSHYREVLPATFVRLLPQEWRLYORGDPAPAFRALVAQCLVCVPW 60

Qy 61 DARRPPAAPSFRQVSCLKEVARYLQLRCERGAKVNLAFGFALDARGGPPPEAFTTSVR 120  
 Db 61 DARRPPAAPSFRQVSCLKEVARYLQLRCERGAKVNLAFGFALDARGGPPPEAFTTSVR 120

Qy 121 SYLPNTVTDALRGSGAWGLLRRGDDVLVHLJARCALFWLVASCAYQVCGPLYOLGA 180  
 Db 121 SYLPNTVTDALRGSGAWGLLRRGDDVLVHLJARCALFWLVASCAYQVCGPLYOLGA 180

Qy 181 ATQARPPPHASGPERLGERAWHNSVREAGVPLGPAPARRGGSASRSLPFPKRPRR 240  
 Db 181 ATQARPPPHASGPERLGERAWHNSVREAGVPLGPAPARRGGSASRSLPFPKRPRR 240

Qy 241 GAAPPERTFGQGSSWAHPGRTRGSDRGFCVWSPARPAEATLEGALSGTRSHPSVG 300  
 Db 241 GAAPPERTFGQGSSWAHPGRTRGSDRGFCVWSPARPAEATLEGALSGTRSHPSVG 300

Qy 301 RQHHAGPPSTSRRPPWDTPCPPTYAETHFLYSSGDEKOLRSPSTLSSLRPSTGTGARRL 360  
 Db 301 RQHHAGPPSTSRRPPWDTPCPPTYAETHFLYSSGDEKOLRSPSTLSSLRPSTGTGARRL 360

Qy 361 VETIFLGSRPWMPGPTRPLPDRYWONRPLFELLGNAQCPGYLLKTHCPRAAVT 420  
 Db 361 VETIFLGSRPWMPGPTRPLPDRYWONRPLFELLGNAQCPGYLLKTHCPRAAVT 420

Qy 421 PAAIGCAREKPGQSYAAPEEEEDTPRRLVQLRQHSSPQVQGYTRACLRLLVPPGLWGS 480  
 Db 421 PAAIGCAREKPGQSYAAPEEEEDTPRRLVQLRQHSSPQVQGYTRACLRLLVPPGLWGS 480

Qy 481 RHNERFLRNTKKFISLGHAKLSQLELTWMSRDCAWLRSPGVPAAEHLREEI 540  
 Db 481 RHNERFLRNTKKFISLGHAKLSQLELTWMSRDCAWLRSPGVPAAEHLREEI 540

Qy 541 LAKFHLMSSVYVLLRSFVYETTFOQNRLFYRKSYWTKQSIGRQLKRVQLRE 600  
 Db 541 LAKFHLMSSVYVLLRSFVYETTFOQNRLFYRKSYWTKQSIGRQLKRVQLRE 600

Qy 601 LSEAEVROHREARPALITSRLRFIPKPDGLRPIVNMYYGARTPRREKRAERTSRVKA 660  
 Db 601 LSEAEVROHREARPALITSRLRFIPKPDGLRPIVNMYYGARTPRREKRAERTSRVKA 660

Qy 661 LFSVINYERARRPGLGASVYLGLDDIHRAWTFLVRVRAODPPPLFYKVDVTGAYDTI 720  
 Db 661 LFSVINYERARRPGLGASVYLGLDDIHRAWTFLVRVRAODPPPLFYKVDVTGAYDTI 720

Qy 721 PQDRITEVASTIILPQNTCYVRAVVOXAHGHYRKAFSKHVSLTLDQPYMRFYAHL 780  
 Db 721 PQDRITEVASTIILPQNTCYVRAVVOXAHGHYRKAFSKHVSLTLDQPYMRFYAHL 780

Qy 781 QETSPRLDAVIEQSSSLNEASSGLFDVFLRMCHAVIRGSKSYVQCGQIPOGSILSTL 840  
 Db 781 QETSPRLDAVIEQSSSLNEASSGLFDVFLRMCHAVIRGSKSYVQCGQIPOGSILSTL 840

Qy 841 LCSLCYGDMEALKFAGIRRGLLRLVDDFLVTPHLTHAKTFRTLVRCVPEYGCVVNL 900  
 Db 841 LCSLCYGDMEALKFAGIRRGLLRLVDDFLVTPHLTHAKTFRTLVRCVPEYGCVVNL 900

Qy 901 RKTIVNFPEVDEALGGTAGVOMPHGLFPWCGLILIDTRTLEVQSDYSSSTARTSRSATL 960  
 Db 901 RKTIVNFPEVDEALGGTAGVOMPHGLFPWCGLILIDTRTLEVQSDYSSSTARTSRSATL 960

Qy 961 NRGPKAAGRMRKRLPGVLRIKCHSLFLDQVNLSQTVCNMNYKILLQAYRPHACVYQLP 1020  
 Db 961 NRGPKAAGRMRKRLPGVLRIKCHSLFLDQVNLSQTVCNMNYKILLQAYRPHACVYQLP 1020

Qy 1021 FHOQYWNPKTFPLRVIYTSITASLCSYLSKAKNAGMSLGAQGAQDPESEAQWLQHAQFLL 1080

Db	1021	FHQQVWNKPTFLRVISDTASLCYSILKAKNAGNSLGIKGAAGPLSSAVQWLCHQAFILL	1080		FT	Peptide	/note= "HLA-A2.1 binding motif"
OY	1081	KLTRHRVTVPLLGSLRATQTLPSRLKPGTTLAEEAANPALSDFKTIILD	1132		FT	Peptide	/note= "HLA-A2.1 binding motif"
Db	1081	KLTRHRVTVPLLGSLRATQTLPSRLKPGTTLAEEAANPALSDFKTIILD	1132		FT	Peptide	926. .934
					FT	Peptide	/note= "HLA-A2.1 binding motif"
					FT	Peptide	934. .942
					FT	Peptide	/note= "HLA-A2.1 binding motif"
					FT	Peptide	969. .977
					FT	Peptide	/note= "HLA-A2.1 binding motif"
					FT	Peptide	988. .996
					FT	Peptide	/note= "HLA-A2.1 binding motif"
					FT	Peptide	1072. .1080
					FT	Peptide	/note= "HLA-A2.1 binding motif"
					FT	Peptide	1079. .1087
					FT	Peptide	/note= "HLA-A2.1 binding motif"
					FT	Peptide	1095. .1103
					FT	Peptide	/note= "HLA-A2.1 binding motif"
					FT	Peptide	1122. .1130
					FT	Peptide	/note= "HLA-A2.1 binding motif"
					XX	W0200160391-A1.	
					PN		
					XX	23-AUG-2001.	
					PD		
					XX	15-FEB-2001;	
					PF	2001WO-US005143.	
					XX		
					PR	15-FEB-2000;	
					XX	2000US-0182685P.	
					PR	15-FEB-2001;	
					XX	2001US-00182685.	
					PA	(REGC ) UNIV CALIFORNIA.	
					PA		
					PI	Zanetti M;	
					XX		
					DR	WPI : 2001-536552/59.	
					XX	Vaccine for initiating and enhancing a cytotoxic T lymphocyte response,	
					PT	PT for treating cancers or tumors or for inducing immune response against	
					XX	tumors, comprises a telomerase reverse transcriptase peptide.	
					XX		
					PS	Disclosure; Fig 5; 52pp; English.	
					XX	The present sequence is that of human telomerase reverse transcriptase	
					CC	CC known binding motifs for the human leukocyte antigen HLA-A2.1 molecule.	
					CC	From an initial panel of about 30 candidate peptides, 2 sequences,	
					CC	denoted p540 (see AAB8772) and p865 (see AAB8773), were examined. The	
					CC	majority of healthy individuals as well as patients with prostate cancer	
					CC	immunised in vitro against these HLA-A2.1 restricted peptides developed	
					CC	hTRT-specific cytotoxic T lymphocytes (CTL). The cancer patients' CTL	
					CC	specifically lysed a variety of HLA-A2+ cancer cell lines such as	
					CC	prostate, breast, colon, lung and melanoma, demonstrating immunological	
					CC	recognition of endogenously-processed hTRT peptides. In vivo immunisation	
					CC	CC of HLA-A2.1 transgenic mice generated a specific CTL response against	
					CC	CC both hTRT peptides. The induction of CTL responses in vitro and in vivo,	
					CC	CC and the susceptibility of tumour cells of various origins by	
					CC	CC hTRT CTL suggest that hTRT could serve as a universal cancer vaccine for	
					CC	CC humans. Thus, a claimed universal vaccine for treating tumours of any	
					CC	CC origin comprises at least 1 hTRT peptide in an amount effective for	
					CC	CC initiating and enhancing a CTL response against cancer cells. The peptide	
					CC	CC is 7-15 amino acid residues in length and may be modified to enhance	
					CC	CC binding to the major histocompatibility complex. Also claimed is a method	
					CC	CC for inducing and enhancing a CTL response against cancer cells, involving	
					CC	CC harvesting blood leucocytes, pulsing with hTRT, and contacting cancer	
					CC	CC cells with the pulsed leucocytes. A method for targeting CTL to tumour	
					CC	CC cells is also claimed, and involves administering a hTRT peptide to a	
					CC	CC mammal, especially a cancer patient	
					XX	Sequence 1132 AA;	
					SQ		
						Query Match 100.0%; Score 5961;	
						Best Local Similarity 100.0%; Pred. No. 0;	
						Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
						Label= P865	



Db	241	GAAPEDPERTPVQGSWAAHPTRGRSDFRGCVVSPARPAEATSLLEGALSGTRSHPSVG	3.00
Qy	301	RQHAGPPSTSRRPRPWDTCPPIYAETKHFLYSSGDXBQLRSPFLSSLRPLTGARRL	3.60
Db	301	RQHAGPPSTSRRPRPWDTCPPIYAETKHFLYSSGDXBQLRSPFLSSLRPLTGARRL	3.60
Qy	361	VETIFIGSRPWPMPGTPLLRLPQYQWQRPFLFELLGNHQAQCPGVLLKTHCPLRRAVT	4.20
Db	361	VETIFIGSRPWPMPGTPLLRLPQYQWQRPFLFELLGNHQAQCPGVLLKTHCPLRRAVT	4.20
Qy	421	PAAGYCAREPKQGSVAAPEEEEDTDPRLVYOLLRQHSSPWQVYCFVRACIIRRLLYPGLWG	4.80
Db	421	PAAGYCAREPKQGSVAAPEEEEDTDPRLVYOLLRQHSSPWQVYCFVRACIIRRLLYPGLWG	4.80
Qy	481	RHNERERFLRNTKKTSLSLGKHAKLSQLETWKMSYRDCAWLRSRPGVCPVPALEHRREEI	5.40
Db	481	RHNERERFLRNTKKTSLSLGKHAKLSQLETWKMSYRDCAWLRSRPGVCPVPALEHRREEI	5.40
Qy	541	LAKTFHMLMSVTVVYELLRSFPFYETTPQRNRLFYRKSVWSKLSQSGIROHLKRYOLRE	6.00
Db	541	LAKTFHMLMSVTVVYELLRSFPFYETTPQRNRLFYRKSVWSKLSQSGIROHLKRYOLRE	6.00
Qy	601	LSEAEVRQHREARPALLTSRLRFLKPDGLRPIVNMDDYVGARTFREKERAERTSRVKA	6.60
Db	601	LSEAEVRQHREARPALLTSRLRFLKPDGLRPIVNMDDYVGARTFREKERAERTSRVKA	6.60
Qy	661	LFSTLNVERARRPGLGASVGLDIDIHAWRTPTVLVRAQDPPPELYFVKVDVTGAYDTI	7.20
Db	661	LFSTLNVERARRPGLGASVGLDIDIHAWRTPTVLVRAQDPPPELYFVKVDVTGAYDTI	7.20
Qy	721	PQDLTEVIASIKPQNTYCVRYYAVVOKAAGHVRKAFKSHSVTSLTDLOPQMRFQV AHL	7.80
Db	721	PQDLTEVIASIKPQNTYCVRYYAVVOKAAGHVRKAFKSHSVTSLTDLOPQMRFQV AHL	7.80
Qy	781	QETSPLRDAVVTEGGSSLINEASSGLPFDYLRFMCCHAVRIGKSYTOCOGIPOGSILSTL	8.40
Db	781	QETSPLRDAVVTEGGSSLINEASSGLPFDYLRFMCCHAVRIGKSYTOCOGIPOGSILSTL	8.40
Qy	841	LCSC1CYGDMENTKLFAIGIRRDGLLRLYDDFLYPTPHLTAKTFLRLVRLGKSYTQCGI	9.00
Db	841	LCSC1CYGDMENTKLFAIGIRRDGLLRLYDDFLYPTPHLTAKTFLRLVRLGKSYTQCGI	9.00
Qy	901	RKTVNPFVDEAEGGTAFVQMPAHLGPWCCLLDTRTLVQSDYYSSARTSIRASLTF	9.60
Db	901	RKTVNPFVDEAEGGTAFVQMPAHLGPWCCLLDTRTLVQSDYYSSARTSIRASLTF	9.60
Qy	961	NRGFKAGNMRKLFGVTLRKLCHSLFDLQVNSLQTYCTNYKILLQAYRFHACYQLP	10.20
Db	961	NRGFKAGNMRKLFGVTLRKLCHSLFDLQVNSLQTYCTNYKILLQAYRFHACYQLP	10.20
Qy	1021	FHQQWNKNPTEFLRVISDTASLCYSILKAKNAGMISLGAKGAGPPESEAVQLCQAFLL	10.80
Db	1021	FHQQWNKNPTEFLRVISDTASLCYSILKAKNAGMISLGAKGAGPPESEAVQLCQAFLL	10.80
Qy	1081	KLTRHRVTVPLIGSLRATAQTQLSRKLPGFTTLTALEAANPALPSDFKTILD	11.32
Db	1081	KLTRHRVTVPLIGSLRATAQTQLSRKLPGFTTLTALEAANPALPSDFKTILD	11.32
Qy	1081	KLTRHRVTVPLIGSLRATAQTQLSRKLPGFTTLTALEAANPALPSDFKTILD	11.32





601	I	S E A F T Q H R E A R P A L I T S R L R F I P K D G L R I V N M D Y V V G A R T P R E K R A B L T S R V K A	6 6 0
661	L	F S V I N Y E R A R R P G L I G A S V I G L D D I H R A W T F V L R V A Q D P P P E L F V K V D T G A Y D T I	7 2 0
661	L	F S V I N Y E R A R R P G L I G A S V I G L D D I H R A W T F V L R V A Q D P P P E L F V K V D T G A Y D T I	7 2 0
721	P	Q D R L I E V I A S I K P O N T Y C V R Y A Y Q K A A G H V R K A F K S H V S T I T D L Q P M R O F V A H L	7 8 0
721	P	Q D R L I E V I A S I K P O N T Y C V R Y A Y Q K A A G H V R K A F K S H V S T I T D L Q P M R O F V A H L	7 8 0
781	Q	Q E T S P R D A V V I E Q S S L N E A S S G L F D V F L R M C H A V R I G K S Y V O C G I F Q G S I L S T L	8 4 0
781	Q	Q E T S P R D A V V I E Q S S L N E A S S G L F D V F L R M C H A V R I G K S Y V O C G I F Q G S I L S T L	8 4 0
841	L	L C S L C Y G D M E N K L F A G I T R D G L I R L Y D D F L I V T P H I T H A K T F L R L T V R G V P E Y G C V N L	9 0 0
841	L	L C S L C Y G D M E N K L F A G I T R D G L I R L Y D D F L I V T P H I T H A K T F L R L T V R G V P E Y G C V N L	9 0 0
901	R	R K T V N P V D E A L G C T A F V O M P A H G I F P W C S I L L I D T R T L V E Q S D S S Y A R T S I R A S I T F	9 6 0
901	R	R K T V N P V D E A L G C T A F V O M P A H G I F P W C S I L L I D T R T L V E Q S D S S Y A R T S I R A S I T F	9 6 0
961	N	N R G F K A G R N M R K L F G V L R L K C H S L F D L Q N S L Q T C T N I Y K I L L Q A Y R P H A C V Q L P	1 0 2 0
961	N	N R G F K A G R N M R K L F G V L R L K C H S L F D L Q N S L Q T C T N I Y K I L L Q A Y R P H A C V Q L P	1 0 2 0
1021	F	F H Q Q V W K N P T F L R V I S T A L C Y S I I K A N G M S I L G A K G A G P L P S E A V O W L C H Q A F L L	1 0 8 0
1021	F	F H Q Q V W K N P T F L R V I S T A L C Y S I I K A N G M S I L G A K G A G P L P S E A V O W L C H Q A F L L	1 0 8 0
1081	K	K L T R H R V T Y P L L G S R T A Q T O L S R K U P G T T L T A L E A A N P A L P S D P K T I L D	1 1 3 2
1081	K	K L T R H R V T Y P L L G S R T A Q T O L S R K U P G T T L T A L E A A N P A L P S D P K T I L D	1 1 3 2

SU115  
PS56676  
ABP56676 standard; protein; 1132 AA.  
ABP56676;

25-MAR-2003 (first entry)

Human telomerase reverse transcriptase protein SEQ ID NO:2

Human; telomerase reverse transcriptase; enzyme; hTERT; chromosome 5;  
vulnary; antiulcer; epithelial cell migration promoter; wound;  
epithelialisation; skin wound; lesion; burn; surgical incision; ulcer;  
epithelial cell; keratinocyte; epidermal; mucosal.

Homo sapiens.  
WO200291999-A2.  
21-NOV-2002.

09-MAY-2002; 2002WO-US014867.

09-MAY-2001; 2001US-02899303P.

(GERO-) GERON CORP.

Jiang X, Chiu C, Harley CB;

WPI; 2003-120591/11.  
N-PSSB; ABZ22474.

Composition for treating wounds and enhancing epithelialization of a skin surface, comprises vector encoding telomerase reverse transcriptase or telomerized epithelial cells on a microparticle or a matrix.

**Disclosure:** Page 32; 68pp; English.

The present invention describes a pharmaceutical composition (I) comprising a vector encoding telomerase reverse transcriptase (TERT) in an excipient or device, or comprises telomeredised epithelial cells on a microparticle or a matrix suitable for topical administration or administration to a wound site. (I) has vulnerable and antiulcer activities and can be used to promote epithelial cell migration. (I) is useful for treating a wound and enhancing epithelialisation of a skin surface. The wound is especially skin wound including acute lesion such as traumatic lesion, burn, or surgical incision, chronic lesion such as chronic venous ulcer, diabetic ulcer or compression ulcer and the wound is further monitored for closure. The telomerase activity or TERT expression is increased in epithelial cells at the site of treatment and also in fibroblasts or endothelial cells at the site of treatment. The epithelial cells are especially keratinocytes. A polynucleotide encoding TERT is useful for the preparation of a medicament for treatment of a wound or an epithelial surface in a human or animal. An epithelial cell with increased telomerase activity or increased expression of TERT is useful for preparation of a medicament for the treatment of a wound in a human or animal. (I) is also useful for treating wounds of other epidermal surfaces including mucosal surfaces such as bronchus, mouth, nose, oesophagus, stomach, or intestine. The present sequence represents human TERT (hTERT), which is given in the exemplification of the present invention. hTERT is located to chromosome 5

Qy	661	LPSVLVNEARRGLGLGSVGLDDIHRAWTRFVLRVRAQDPPFLFYKVDVTGAYDTI	720
Db	661	LPSVLVNEARRGLGLGSVGLDDIHRAWTRFVLRVRAQDPPFLFYKVDVTGAYDTI	720
Qy	721	PODRLETVIASIKPQNTYCVRYYAVQKAAGHGVRKAFKSHVSTLTDLOPYMRFV AHL	780
Db	721	PODRLETVIASIKPQNTYCVRYYAVQKAAGHGVRKAFKSHVSTLTDLOPYMRFV AHL	780
Qy	781	QETSPSLRDAVIEQSSSLNEASSCGLDFYPLRFMCHAVTRGKSYVQCCGIPQGSILS TL	840
Db	781	QETSPSLRDAVIEQSSSLNEASSCGLDFYPLRFMCHAVTRGKSYVQCCGIPQGSILS TL	840
Qy	841	LCSLCYGDMENTKLFGAIGTRDGLLRLVDDFLLTPTHLTHAKTFITRLVRGVPE TGCVVNL	900
Db	841	LCSLCYGDMENTKLFGAIGTRDGLLRLVDDFLLTPTHLTHAKTFITRLVRGVPE TGCVVNL	900
Qy	901	RKTUVNPFVEDAEGTAFVOMPAHGLFPWCGLLIDDTRTLLEVSDSSYSTARTSIRASLTF	960
Db	901	RKTUVNPFVEDAEGTAFVOMPAHGLFPWCGLLIDDTRTLLEVSDSSYSTARTSIRASLTF	960
Qy	961	NRGFKAGRNMRRKLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVL QLP	1020
Db	961	NRGFKAGRNMRRKLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVL QLP	1020
Qy	1021	PHQQWVKQPTFFLRV1SDTASLCYSILKAKNAGMSLGAKGAAGPSEAVQWLCHQAFJL	1080
Db	1021	PHQQWVKQPTFFLRV1SDTASLCYSILKAKNAGMSLGAKGAAGPSEAVQWLCHQAFJL	1080
Qy	1081	KLTZRHRRTYVPLLSRATQOTLSRKPLGTTLAEEAANPALPSDFEKTLD	1132
Db	1081	KLTZRHRRTYVPLLSRATQOTLSRKPLGTTLAEEAANPALPSDFEKTLD	1132

Search completed: January 10, 2005, 17:34:53  
Job time : 175 sec

Scoring table:	BLOSUM62	Alignments	
Gapopen:	10.0	Gapext:	0.5
Searched:	1825181 seqs, 575374646 residues		
Total number of hits satisfying chosen parameters:	1825181		
Minimum DB seq length:	0		
Maximum DB seq length:	2000000000		
Post-processing:	Minimum Match 0%		
	Maximum Match 100%		
	Listing first 45 summaries		
Database :	UniProt_02: 1: uniprot_sprot: 2: uniprot_trembl: *		
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	5583.5	100.0 1132 1 TERT HUMAN QBN46	014746 homo sapien
2	4052.0	93.7 1069 2 QBN6C3	08ng46 homo sapien
3	3628.0	68.0 807 2 QBNG38	Q8n6c3 homo sapien
4	3505.0	66.6 795 2 Q9QXZ4	Q8ng46 homo sapien
5	3505.0	60.9 1128 2 Q9QXZ4	Q9qxz4 mesocricetus auratus
6	2825.4	58.8 1122 1 TERT MOUSE Q9UBR6	Q9qxz4 mesocricetus auratus
7	2590.4	47.4 524 2 Q9UBR6	Q9ubr6 homo sapien
8	2590.4	43.4 1346 2 Q6RDB0	Q6rdb0 gallus gallus
9	2316.5	43.4 1346 2 AAS75793	Aas75793 gallus gallus
10	2207.5	38.9 1191 2 Q9DE32	Q9de32 xenopus laevis
11	2016.0	37.0 523 2 Q94807	Q94807 homo sapien
12	1373.0	33.8 575 2 Q9JK99	Q9jk99 rattus norvegicus
13	1373.0	23.0 514 2 Q9R266	Q9r266 mus musculus
14	724.5	12.2 1123 2 Q9SE99	Q9se99 arribidopsis
15	724.5	12.2 - 1123 2 Q9SPU7	Q9spu7 arribidopsis
16	688.0	11.5 1259 2 Q9AU13	Q9au13 oryza sativa
17	654.5	11.0 1261 2 Q8LKWO	Q8lkwo oryza sativa
18	594.0	10.0 988 1 TEXT SCPO	Q13339 schizosaccharomyces pombe
19	478.0	8.0 1032 2 Q7ZIL1	Q7zil1 eukaryotes
20	474.0	8.0 1032 2 QBMUB3	Q8mbm3 eukaryotes
21	469.5	7.9 939 2 Q7SD71	Q7sd71 neurospora crassa
22	450.0	7.5 85 2 Q9UN56	Q9un56 homo sapiens
23	450.0	7.5 940 2 Q6C9D0	Q6c9d0 yarrowia lipolytica
24	449.0	7.5 116 2 Q8QSUS	Q8qsus rattus norvegicus
25	448.5	7.5 1031 1 TERT EUPAE	Q00939 eukaryotes
26	441.0	7.4 1032 2 Q7ZIL0	Q7zil0 eukaryotes
27	408.0	6.8 823 2 Q8SQQ0	Q8sqq0 encephalitozoon cuniculi
28	397.0	6.7 104 2 Q9JLM1	Q9jlm1 mus musculus
29	395.5	6.6 1135 2 Q8IBZ7	Q8ibz7 sterkeilla
30	395.0	6.6 1132 1 TERT OXYTR	Q76332 oxytricha t
31	395.0	6.6 1132 2 AAN87865	Aan87865 sterkeilla

RX	PubMed=11029039;	Db	241 GAAPEPERTPVGGQSWAHFGRTGFDPSDRGFCVUSPARPAAEATSLEGALSGTRSHPSVG 300
RA	Beattie T.L., Zhou W., Robinson M.O., Harrington L.;	Oy	301 ROHHAGPPETSRRPREWDPDPCPPYTAETKHELYSGDKEQLRPFLLSSLRPSTLGARRL 360
RT	"Polymerization detects within human telomerase are distinct from telomerase RNA and TEPII binding."	Db	301 RQHAGPPETSRRPREWDPDPCPPYTAETKHELYSGDKEQLRPFLLSSLRPSTLGARRL 360
CC	-1: FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for the replication of chromosome termini in most eukaryotes. It elongates telomeres. It is a reverse transcriptase that adds simple sequence repeats to chromosome ends by copying a template sequence within the RNA component of the enzyme.	Qy	361 VETIPLGSRPWMPPTPRPLPRIPLQRYWMQRPLFELLGNHAQCYGVLLKTHCPLRAVT 420
CC	-1: SUBUNIT: Component of the telomerase ribonucleoprotein complex at least composed of TSP1, EST1A, POT1 and a telomerase RNA template component (TER). Interacts with PINK1.	Db	361 VETIPLGSRPWMPPTPRPLPRIPLQRYWMQRPLFELLGNHAQCYGVLLKTHCPLRAVT 420
CC	-1: SUBCELLULAR LOCATION: Nuclear.	Qy	421 PAAVGCAREKPKQGVAAPPBEDTPRLVQLLRRHSSPQVYGVRACLRLVPGLWGS 480
CC	-1: DISEASE: Activation of telomerase has been implicated in cell immortalization and cancer cell pathogenesis.	Db	421 PARGVCAEKPKQGVAAPPBEDTPRLVQLLRRHSSPQVYGVRACLRLVPGLWGS 480
CC	-1: SIMILARITY: Belongs to the reverse transcriptase family.	Qy	481 RHNERFLRINTKKFTISLGKHAKLSQLETWKMSVYRDCAWLRSSEFGVGCPAAEHLREI 540
CC	CC - This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	Db	481 RHNERFLRINTKKFTISLGKHAKLSQLETWKMSVYRDCAWLRSSEFGVGCPAAEHLREI 540
CC	DR	Qy	541 LAKEFLHWLMSVYYVELLSFFYTETTFOKNRLFYRKSVWMSKLQSISIGTRQHLKVRQLRE 600
CC	EMBL	Db	541 LAKEFLHWLMSVYYVELLSFFYTETTFOKNRLFYRKSVWMSKLQSISIGTRQHLKVRQLRE 600
CC	EMBL	Qy	601 LSEAEVROHREAPALLTSRLRFPKPGPLRPIVMDVYVGARTFRERKAERTSRYKA 660
CC	EMBL	Db	601 LSEAEVROHREAPALLTSRLRFPKPGPLRPIVMDVYVGARTFRERKAERTSRYKA 660
CC	DR	Qy	661 LFSTLVNTERARRPELLGASVLGQDPPPELYFVKVDVGTAYDTI 720
CC	EMBL	Db	661 LFSTLVNTERARRPELLGASVLGQDPPPELYFVKVDVGTAYDTI 720
CC	EMBL	Qy	721 PQDLTEIASIKPQNTYCVERRAYVYOKAAHGHVRKAFKSHSYTLTDLQPYMRQFV AHL 780
CC	EMBL	Db	721 PQDLTEIASIKPQNTYCVERRAYVYOKAAHGHVRKAFKSHSYTLTDLQPYMRQFV AHL 780
CC	DR	Qy	781 QETSPRLDAVVIQSSSLNEASSGLFDVFLRMCHAVHVRGKSYVQOCQIPQGSILSTL 840
CC	GO; GO:0000781; DR	Db	781 QETSPRLDAVVIQSSSLNEASSGLFDVFLRMCHAVHVRGKSYVQOCQIPQGSILSTL 840
CC	GO; GO:0042162; F:telomeric DNA binding; TAS.	Qy	841 LCS:CYGDMENTKLFAIGIRRDGLLRLVDDFLLYPHLTHAKTFLRTLTYRGVPYGVNL 900
CC	DR	Db	841 LCS:CYGDMENTKLFAIGIRRDGLLRLVDDFLLYPHLTHAKTFLRTLTYRGVPYGVNL 900
CC	PRINTS; PRO1345; F:telomeric template RNA reverse transcriptas...	Qy	901 RKTIVNFNPVEDEAIGGTAFVOMPAHGLFPWCGLLDDTRLEVSODYSSYARTSTRASLT F 960
CC	DR	Db	901 RKTIVNFNPVEDEAIGGTAFVOMPAHGLFPWCGLLDDTRLEVSODYSSYARTSTRASLT F 960
CC	InterPro; IPR003545; Telomerase_RT.	Qy	960 FHOQWKAQPTFLQVVISDDASLCSYLSILKAKNNGMSLGAQGPPLPSEAQMULHQAFPL 1080
CC	DR	Db	960 FHOQWKAQPTFLQVVISDDASLCSYLSILKAKNNGMSLGAQGPPLPSEAQMULHQAFPL 1080
CC	Pfam; PF00078; RVT; 1.	Qy	961 NRGFKAGRMRRKLFGVLRLKCHSFLDQNSLQTCTNIKILLQAYRFHACVQLQP 1020
CC	PRINTS; PRO1345; TELOMERASeRT.	Db	961 NRGFKAGRMRRKLFGVLRLKCHSFLDQNSLQTCTNIKILLQAYRFHACVQLQP 1020
KW	DNA-binding; Nuclear protein; Ribonucleoprotein; RNA-directed DNA polymerase; Telomerase; Transferase.	Qy	1021 PHQCVWKNPTEFLRVISDPTASLCSYLSILKAKNNGMSLGAQGPPLPSEAQMULHQAFPL 1080
MUTAGEN	868 868 D->A: Loss of telomerase activity.	Db	1021 PHQCVWKNPTEFLRVISDPTASLCSYLSILKAKNNGMSLGAQGPPLPSEAQMULHQAFPL 1080
MUTAGEN	868 869 D->A: Loss of telomerase activity.	Qy	1081 KLTFRHRVTVPLGLSRLTAOTLSRKLFQGTTLTALEAAANPALPSDFKTIID 1132
MUTAGEN	869 869 D->A: Loss of telomerase activity.	Db	1081 KLTFRHRVTVPLGLSRLTAOTLSRKLFQGTTLTALEAAANPALPSDFKTIID 1132
MUTAGEN	712 712 D->A: Loss of telomerase activity.	Qy	1081 KLTFRHRVTVPLGLSRLTAOTLSRKLFQGTTLTALEAAANPALPSDFKTIID 1132
SEQUENCE	516 516 D -> G (in Ref. 2).	Db	1081 KLTFRHRVTVPLGLSRLTAOTLSRKLFQGTTLTALEAAANPALPSDFKTIID 1132
SQ	1132 AA; 112996 MW; 94E33469c4CA3340 CRC64;	Qy	RESULTS 2
		Qy	QNG46 ID QNG46 PRELIMINARY; PRT; 1069 AA.
		Db	QNG46 AC QNG46; DT 01-OCT-2002 (TREMBLrel. 22, Created)
		Qy	DB 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
		Db	DB 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
		Qy	DB Telomerase reverse transcriptase.
		Qy	GN Name=htERT Homo sapiens (Human).
		Qy	OS OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
		Db	OS OC Bivalvia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
		Qy	NCBI_TaxID=9606; NCBI_TaxID=9606;



Db	241	GAPEPERBERTPVQGGSWAHPGRTRGPSPRGFCVVSAPARAEATSLEGALSSTRHSHPSVG	300		Db	61	DARPPPAAPSFRQVSCLKELVARYLQRLLCERGAKNLAFGFALLDGARGGPPEAFTTSVR	120
Qy	301	ROHHAGPPESTSRRPRPDTCPBPVYATETKHFELLYSSCDEQLRSPSFESSLRRPSLTCARPL	360	Qy	121	SYLDNTVTALRGGAGAWGILLRRGGDVLVHLARCAFLVLFVSCAYQVCGPPLYOLGA	180	
Db	301	ROHHAGPPESTSRRPRPDTCPBPVYATETKHFELLYSSCDEQLRSPSFESSLRRPSLTCARPL	360	Db	121	SYLPNTVTALRGGAGAWGILLRRGGDVLVHLARCAFLVSCAYQVCGPPLYOLGA	180	
Qy	361	VETIFLSSRPMPGTTPRLPRLPRLPQLPYQMRPFLFELIGNHQACPYGVLLKTHCPRAVTT	420	Qy	181	ATQARPPhASGPRLGCERAVNHVSREAGVPLGLPAGFARRGGSASRSLPLPKRPRR	240	
Db	361	VETIFLSSRPMPGTTPRLPRLPRLPQLPYQMRPFLFELIGNHQACPYGVLLKTHCPRAVTT	420	Db	181	ATQARPPhASGPRLGCERAVNHVSREAGVPLGLPAGFARRGGSASRSLPLPKRPRR	240	
Qy	421	PAAGVCAREKPQGSVAPEEEEDTPRRLVQLLRQHSSPWQYGFYRACLERLVPPLWGS	480	Qy	241	GAAPEPERTPVQGGSWAHPGRTRGPSPDRGFCVUSPARAAEATSLEGALSGTRHSHPSVG	300	
Db	421	PAAGVCAREKPQGSVAPEEEEDTPRRLVQLLRQHSSPWQYGFYRACLERLVPPLWGS	480	Db	241	GAAPEPERTPVQGGSWAHPGRTRGPSPDRGFCVUSPARAAEATSLEGALSGTRHSHPSVG	300	
Qy	481	RHNERFLRNLTKKKFISLGKAHLKLSLQFLPTWKMSVRCDAWLRRSPGCVPAAEHLRREEI	540	Qy	301	ROHNGPPESTSRRPRPDTCPBPVYAEKHFELYSGGDEQLRSPFLASLRSPLTGARRL	360	
Db	481	RHNERFLRNLTKKKFISLGKAHLKLSLQFLPTWKMSVRCDAWLRRSPGCVPAAEHLRREEI	540	Db	301	ROHAGPPESTSRRPRPDTCPBPVYAEKHFELYSGGDEQLRSPFLASLRSPLTGARRL	360	
Qy	541	LAKFLHMLMSYYVVELRSFFYVTEETFOQNRLFFYRKSYNSKLSQSIGIRQLKRVQRLR	600	Qy	361	VETFLGSSPRWMPMTPRPLPRLPRLPQLPYWONRPLFELJUNHAQCPYGVLLKTHCPRLRAVT	420	
Db	541	LAKFLHMLMSYYVVELRSFFYVTEETFOQNRLFFYRKSYNSKLSQSIGIRQLKRVQRLR	600	Db	361	VETFLGSSPRWMPMTPRPLPRLPRLPQLPYWONRPLFELJUNHAQCPYGVLLKTHCPRLRAVT	420	
Qy	601	LSEAEVHQHREARPALLTSRLRFIPKPGDRPITVNDYVYGARTPRREKAERLTSVKA	660	Qy	421	PAAGVCAREKPQGSVAAPEEEEDTPRRLVQLLRQHSSPWQYGFVACLRLRYPGLWGS	480	
Db	601	LSEAEVHQHREARPALLTSRLRFIPKPGDRPITVNDYVYGARTPRREKAERLTSVKA	660	Db	421	PAAGVCAREKPQGSVAAPEEEEDTPRRLVQLLRQHSSPWQYGFVACLRLRYPGLWGS	480	
Qy	661	LFSVLNTERARRPGLIGASVILGLDDHRAWTFTVLRQAODPPPELYFVVDVGTAYDTI	720	Qy	481	RHNRERFLRNLTKKFIISLGKAHLKLSLQFLTWKMSVRCDAWLRSPLGCVPAAEHLRREEI	540	
Db	661	LFSVLNTERARRPGLIGASVILGLDDHRAWTFTVLRQAODPPPELYFVVDVGTAYDTI	720	Db	481	RHNRERFLRNLTKKFIISLGKAHLKLSLQFLTWKMSVRCDAWLRSPLGCVPAAEHLRREEI	540	
Qy	721	PQDRLTVEIASIPIKPontyCYRRAYVQKAAGHGHYRKAFKSHV	763	Qy	541	LAKFLHMLMSYYVVELRSFFYVTEETFOQNRLFFYRKSVWSKLQSTGIRQLKRVQRLR	600	
Db	721	PQDRLTVEIASIPIKPontyCYRRAYVQKAAGHGHYRKAFKSHV	763	Db	541	LAKFLHMLMSYYVVELRSFFYVTEETFOQNRLFFYRKSVWSKLQSTGIRQLKRVQRLR	600	
Qy	[1]	SEQUENCE FROM N.A.		Qy	601	LSEAEVHQHREARPALLTSRLRFIPKPGDRPITVNDYVVGARTFRREKAERLTSVKA	660	
RN	[1]	SEQUENCE FROM N.A.		Db	601	LSEAEVHQHREARPALLTSRLRFIPKPGDRPITVNDYVVGARTFRREKAERLTSVKA	660	
RC	Q8NG38	PRELIMINARY;	PRT;	Qy	661	LFSLVNYTERARRPGLIGASVILGLDDHRAWTFTVLRQAODPPPELYFVVDVGTAYDTI	720	
AC	Q8NG38	PRELIMINARY;	PRT;	Db	661	LFSLVNYTERARRPGLIGASVILGLDDHRAWTFTVLRQAODPPPELYFVVDVGTAYDTI	720	
DT	01-OCT-2002	(TREMBLref. 22, Created)		Qy	721	PQDLTEVIASIIKPontyCYRYAYVQKAAGHGHYRKAFKSHV	763	
DT	01-OCT-2002	(TREMBLref. 22, Last sequence update)		Db	721	PQDLTEVIASIIKPontyCYRYAYVQKAAGHGHYRKAFKSHV	763	
DB	01-OCT-2003	(TREMBLref. 25, Last annotation update)		Qy	711	--DRLTEVIASIIKPontyCYRYAYVQKAAGHGHYRKAFKSHV	763	
GN	NAME=ERT;			Db	711	--DRLTEVIASIIKPontyCYRYAYVQKAAGHGHYRKAFKSHV	763	
OS	Homo sapiens (Human)			Qy	SEQUENCE FROM N.A.			
CC	Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;			Qy	SEQUENCE FROM N.A.			
NCBI_TAXID=9606;				Qy	SEQUENCE FROM N.A.			
OX				Qy	SEQUENCE FROM N.A.			
RN				Qy	SEQUENCE FROM N.A.			
RP				Qy	SEQUENCE FROM N.A.			
RC				Qy	SEQUENCE FROM N.A.			
TISSUE=Stomach;				Qy	SEQUENCE FROM N.A.			
RA				Qy	SEQUENCE FROM N.A.			
RL				Qy	SEQUENCE FROM N.A.			
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.				Qy	SEQUENCE FROM N.A.			
EMBL, AB08695Q, BAC11015.1;				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
GO; GO:0005634; -E:nucleus; IEA.				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
GO; GO:0003677; F:DNA binding; IEA.				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
InterPro: IPR003545; telomerase; RT.				Qy	SEQUENCE FROM N.A.			
PRINTS: PR01365; TELOMERASeRT.				Qy	SEQUENCE FROM N.A.			
KW				Qy	SEQUENCE FROM N.A.			
RNA-directed DNA polymerase.				Qy	SEQUENCE FROM N.A.			
SEQUENCE 795 AA;	88964 MW;	6BEACBA6D1A2E8CB CRC64;		Qy	SEQUENCE FROM N.A.			
Query Mat 66.6%; Score 3973; DB 2; Length 795;				Qy	SEQUENCE FROM N.A.			
Best Local Similarity 98.4%; Pred. No. 7-240;				Qy	SEQUENCE FROM N.A.			
Matches 751; Conservative 0; Mismatches 0; Indels 12; Gaps 1;				Qy	SEQUENCE FROM N.A.			
RC	1 MPRAPCRATVSLRSHREVLPLATFVRLLGPQGWRLVQGDPAFAFLVALQAQLCVCW	60		Qy	SEQUENCE FROM N.A.			
AC	1 MPRAPCRATVSLRSHREVLPLATFVRLLGPQGWRLVQGDPAFAFLVALQAQLCVCW	60		Qy	SEQUENCE FROM N.A.			
DT	01-MAY-2000 (TREMBLref. 13, Created)			Qy	SEQUENCE FROM N.A.			
DR	01-MAY-2000 (TREMBLref. 13, Last sequence update)			Qy	SEQUENCE FROM N.A.			
DT	01-OCT-2003 (TREMBLref. 25, Last annotation update)			Qy	SEQUENCE FROM N.A.			
DB	Telomerase catalytic subunit.			Qy	SEQUENCE FROM N.A.			
OS	Mesocricetus auratus (Golden hamster).			Qy	SEQUENCE FROM N.A.			
CC	Mesocricetus auratus (Golden hamster).			Qy	SEQUENCE FROM N.A.			
NCBI_TAXID=1036;				Qy	SEQUENCE FROM N.A.			
OX				Qy	SEQUENCE FROM N.A.			
RN				Qy	SEQUENCE FROM N.A.			
RP				Qy	SEQUENCE FROM N.A.			
RC				Qy	SEQUENCE FROM N.A.			
TISSUE=Stomach;				Qy	SEQUENCE FROM N.A.			
RA				Qy	SEQUENCE FROM N.A.			
RL				Qy	SEQUENCE FROM N.A.			
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.				Qy	SEQUENCE FROM N.A.			
EMBL, AB08695Q, BAC11015.1;				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
GO; GO:0005634; -E:nucleus; IEA.				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
GO; GO:0003677; F:DNA binding; IEA.				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
InterPro: IPR003545; telomerase; RT.				Qy	SEQUENCE FROM N.A.			
PRINTS: PR01365; TELOMERASeRT.				Qy	SEQUENCE FROM N.A.			
KW				Qy	SEQUENCE FROM N.A.			
RNA-directed DNA polymerase.				Qy	SEQUENCE FROM N.A.			
SEQUENCE 795 AA;	88964 MW;	6BEACBA6D1A2E8CB CRC64;		Qy	SEQUENCE FROM N.A.			
Query Mat 66.6%; Score 3973; DB 2; Length 795;				Qy	SEQUENCE FROM N.A.			
Best Local Similarity 98.4%; Pred. No. 7-240;				Qy	SEQUENCE FROM N.A.			
Matches 751; Conservative 0; Mismatches 0; Indels 12; Gaps 1;				Qy	SEQUENCE FROM N.A.			
RC	1 MPRAPCRATVSLRSHREVLPLATFVRLLGPQGWRLVQGDPAFAFLVALQAQLCVCW	60		Qy	SEQUENCE FROM N.A.			
AC	1 MPRAPCRATVSLRSHREVLPLATFVRLLGPQGWRLVQGDPAFAFLVALQAQLCVCW	60		Qy	SEQUENCE FROM N.A.			
DT	01-MAY-2000 (TREMBLref. 13, Created)			Qy	SEQUENCE FROM N.A.			
DR	01-MAY-2000 (TREMBLref. 13, Last sequence update)			Qy	SEQUENCE FROM N.A.			
DB	Telomerase catalytic subunit.			Qy	SEQUENCE FROM N.A.			
OS	Mesocricetus auratus (Golden hamster).			Qy	SEQUENCE FROM N.A.			
CC	Mesocricetus auratus (Golden hamster).			Qy	SEQUENCE FROM N.A.			
NCBI_TAXID=1036;				Qy	SEQUENCE FROM N.A.			
OX				Qy	SEQUENCE FROM N.A.			
RN				Qy	SEQUENCE FROM N.A.			
RP				Qy	SEQUENCE FROM N.A.			
RC				Qy	SEQUENCE FROM N.A.			
TISSUE=Stomach;				Qy	SEQUENCE FROM N.A.			
RA				Qy	SEQUENCE FROM N.A.			
RL				Qy	SEQUENCE FROM N.A.			
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.				Qy	SEQUENCE FROM N.A.			
EMBL, AB08695Q, BAC11015.1;				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
GO; GO:0005634; -C:nucleus; IEA.				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
GO; GO:0003677; F:DNA binding; IEA.				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
InterPro: IPR003545; telomerase; RT.				Qy	SEQUENCE FROM N.A.			
PRINTS: PR01365; TELOMERASeRT.				Qy	SEQUENCE FROM N.A.			
KW				Qy	SEQUENCE FROM N.A.			
RNA-directed DNA polymerase.				Qy	SEQUENCE FROM N.A.			
SEQUENCE 795 AA;	88964 MW;	6BEACBA6D1A2E8CB CRC64;		Qy	SEQUENCE FROM N.A.			
Query Mat 66.6%; Score 3973; DB 2; Length 795;				Qy	SEQUENCE FROM N.A.			
Best Local Similarity 98.4%; Pred. No. 7-240;				Qy	SEQUENCE FROM N.A.			
Matches 751; Conservative 0; Mismatches 0; Indels 12; Gaps 1;				Qy	SEQUENCE FROM N.A.			
RC	1 MPRAPCRATVSLRSHREVLPLATFVRLLGPQGWRLVQGDPAFAFLVALQAQLCVCW	60		Qy	SEQUENCE FROM N.A.			
AC	1 MPRAPCRATVSLRSHREVLPLATFVRLLGPQGWRLVQGDPAFAFLVALQAQLCVCW	60		Qy	SEQUENCE FROM N.A.			
DT	01-MAY-2000 (TREMBLref. 13, Created)			Qy	SEQUENCE FROM N.A.			
DR	01-MAY-2000 (TREMBLref. 13, Last sequence update)			Qy	SEQUENCE FROM N.A.			
DB	Telomerase catalytic subunit.			Qy	SEQUENCE FROM N.A.			
OS	Mesocricetus auratus (Golden hamster).			Qy	SEQUENCE FROM N.A.			
CC	Mesocricetus auratus (Golden hamster).			Qy	SEQUENCE FROM N.A.			
NCBI_TAXID=1036;				Qy	SEQUENCE FROM N.A.			
OX				Qy	SEQUENCE FROM N.A.			
RN				Qy	SEQUENCE FROM N.A.			
RP				Qy	SEQUENCE FROM N.A.			
RC				Qy	SEQUENCE FROM N.A.			
TISSUE=Stomach;				Qy	SEQUENCE FROM N.A.			
RA				Qy	SEQUENCE FROM N.A.			
RL				Qy	SEQUENCE FROM N.A.			
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.				Qy	SEQUENCE FROM N.A.			
EMBL, AB08695Q, BAC11015.1;				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
GO; GO:0005634; -C:nucleus; IEA.				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
GO; GO:0003677; F:DNA binding; IEA.				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
InterPro: IPR003545; telomerase; RT.				Qy	SEQUENCE FROM N.A.			
PRINTS: PR01365; TELOMERASeRT.				Qy	SEQUENCE FROM N.A.			
KW				Qy	SEQUENCE FROM N.A.			
RNA-directed DNA polymerase.				Qy	SEQUENCE FROM N.A.			
SEQUENCE 795 AA;	88964 MW;	6BEACBA6D1A2E8CB CRC64;		Qy	SEQUENCE FROM N.A.			
Query Mat 66.6%; Score 3973; DB 2; Length 795;				Qy	SEQUENCE FROM N.A.			
Best Local Similarity 98.4%; Pred. No. 7-240;				Qy	SEQUENCE FROM N.A.			
Matches 751; Conservative 0; Mismatches 0; Indels 12; Gaps 1;				Qy	SEQUENCE FROM N.A.			
RC	1 MPRAPCRATVSLRSHREVLPLATFVRLLGPQGWRLVQGDPAFAFLVALQAQLCVCW	60		Qy	SEQUENCE FROM N.A.			
AC	1 MPRAPCRATVSLRSHREVLPLATFVRLLGPQGWRLVQGDPAFAFLVALQAQLCVCW	60		Qy	SEQUENCE FROM N.A.			
DT	01-MAY-2000 (TREMBLref. 13, Created)			Qy	SEQUENCE FROM N.A.			
DR	01-MAY-2000 (TREMBLref. 13, Last sequence update)			Qy	SEQUENCE FROM N.A.			
DB	Telomerase catalytic subunit.			Qy	SEQUENCE FROM N.A.			
OS	Mesocricetus auratus (Golden hamster).			Qy	SEQUENCE FROM N.A.			
CC	Mesocricetus auratus (Golden hamster).			Qy	SEQUENCE FROM N.A.			
NCBI_TAXID=1036;				Qy	SEQUENCE FROM N.A.			
OX				Qy	SEQUENCE FROM N.A.			
RN				Qy	SEQUENCE FROM N.A.			
RP				Qy	SEQUENCE FROM N.A.			
RC				Qy	SEQUENCE FROM N.A.			
TISSUE=Stomach;				Qy	SEQUENCE FROM N.A.			
RA				Qy	SEQUENCE FROM N.A.			
RL				Qy	SEQUENCE FROM N.A.			
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.				Qy	SEQUENCE FROM N.A.			
EMBL, AB08695Q, BAC11015.1;				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
GO; GO:0005634; -C:nucleus; IEA.				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
GO; GO:0003677; F:DNA binding; IEA.				Qy	SEQUENCE FROM N.A.			
DR				Qy	SEQUENCE FROM N.A.			
GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.				Qy	SEQUENCE FROM N.A.			
DR				Qy</				

DR	GO:00016740; F:transferase activity; IEA.	Qy	871 LLVTPHILTHAKTFLRLTVRGVPEYGCVNLRKTVNNFPVEDALGGTAFYQMPAHGLFPW 930
DR	GO:0006278; P:RNA-dependent DNA replication; IEA.	Db	867 LLVTPHILQAAEFLARLVRGPIPEYGMINLQRKTVNNFPVDAGTLDETAFLPACLFPW 926
DR	Interrvo; IPR000477; RVTse.	Qy	931 CGLLLDTTRLEVQDYYSSARTSIRASLTFNRGKAGRNNMRKLFGVYLKCHSLFDLQ 990
DR	Pfam; PF00078; RVT; 1.	Db	927 CGLLLDTQTLLEVLCDDTYGARYTSIKASLTQFTKAGRNNRQKLAVLRLKCHSLFDLQ 986
DR	PRINTS; PRO1365; TELOMERASE.	Qy	991 VNSLQTVCTNLYK1LQAYRFHACVQLQPLPHQWKNPTEFLRVISDTASLCYSLIKAK 1050
RW	RNA-directed DNA polymerase; Transferase.	Qy	991 VNSLQTVCTNLYK1LQAYRFHACVQLQPLPHQWKNPTEFLRVISDTASLCYSLIKAK 1050
SQ	SEQUENCE 1128 AA; 12893 MW; 1D4F81249012174E CRC64;	Db	987 MNSLQIVCINTYK1FLQARFHACALQLPDQHVRKNPAFFLSISNIASCCYSILVK 1046
Query Match	Score 3628; DB 2; Length 1128;	Qy	987 MNSLQIVCINTYK1FLQARFHACALQLPDQHVRKNPAFFLSISNIASCCYSILVK 1046
Best Local Similarity	60.9%; Pred. No. 4.5e-218;	Db	987 MNSLQIVCINTYK1FLQARFHACALQLPDQHVRKNPAFFLSISNIASCCYSILVK 1046
Matches	736; Conservative 124; Mismatches 238; Indels 64; Gaps 16;	Qy	1051 NAGMSIAGKAAGLPPLSEAOVHLCHOAFLKLTRHVTYPLLGSLRTAQTLSRKLPGT 1110
Qy	1 MPRAPRGRAYRSLLSHREYREVPLAFVRRRLGPQGKRLVORGDPAAFLRVAQCLVCVPW 60	Db	1047 NAGMTLKAKGAGSGSFPEAFLRWAFLQAGSIVKCLGPRTAQKQLCRKLPR 1106
Db	1 MPRAPRGRAYRSLLSHREYREVPLAFVRRRLGPQGKRLVORGDPAAFLRVAQCLVCVPW 60	Qy	1111 TLTALEAAANPALPSDFKTID 1132
Qy	61 DARPPPAPSPFQVSCKELVARVILQRLCERGAKVNLAFGFLALDARGGPPEAFTTSVR 120	Db	1107 TMALLETAADPALSTDFTQITID 1128
Db	61 DSQPPPAPDSLPHQVSSKELVARVILQRLCERGVNLTFGFALLINGAQGQDPMTFTTSVR 120		
Qy	121 SYLPNTYTDALRGSGAWGLLIRRGGDVLVHLLARCAFLVAPSCAYQVCGPPLYQOLGA 180		RESULT 6
Db	121 SYLPNTYTDIURGVGMLLNRVGDLLVHLLARCAFLVAPSCAYQVCGPPLYQICA 180		TERT MOUSE
Qy	181 ATQARPP-PHAGSPRRLG-----CERAMNHSHREAGYPLGLPAGGARRGGSSAARS 231		ID TERT MOUSE STANDARD
Db	181 TAETWPVPSRLYRPTPFRVGFRNFTHLGSHTHRVRNNSHQEANRKPPLIPSREAKRSLSITNRS 240		AC 070372; O35432;
Qy	232 LPLPKRERGGAPEPRTPVCGSWAHGPRTRGPSPDGFCTVSPAR----PAAEATSLLEG 287		DT 30-MAY-2000 (Rel. 39, Created)
Db	241 VPPSKXKRCDAPLREKGPTQRA----VPTPSDKTW-VPNPAKSHAVPISRTK-ED 291		DT 05-JUL-2004 (Rel. 44, Last annotation update)
Qy	288 ALSGTRHSHPSVYGRQ---HHAGPPSTS-RP-----RPWDIPCPYPAETKHFYLS 334		DB Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit).
Db	292 LSSGVK--AEGRSRSSVCYHKHPSSSTLQSPBLQCNQAFLQRP-----YTETKRFYLS 341		DE subunit).
Qy	335 -SGDKEQLQRPSPFLSSLRPSELTTGARRLVETFLGSRPWPMPGTPRRLPRLPORYWQMRPLF 393		GN Name-Tert;
Db	342 REGGRERLNPSPFLNNIQLQPSLUTGARNLVEILFLGHRPRTSPLCGRRLSKEYWQMRPLF 401		OS Mus musculus (Mouse).
Qy	394 LEGLGNAQCPCYGVLKJLKHCPLRATAVPAAGWCAREKPGQSVAAPEEEDTPRRLVQLLRR 453		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus .
Db	402 QQLVNHARCPYVRLJSHCRFTAHHQVAGAL----NTTSPQRUNMLLR 447		NCBI TaxID=10030;
Qy	454 OHSSPNCVNYGFVRAFLRVLYPGLMSRHNERRFLNTKEPISLKSXAKLSSLQELTWKMS 513		OX RN [1]
Db	448 LHSSPQVQYGFQACYQKLVPGLMSRHNORFFKVNKRKEPISLGSXAKLSSLQELTWKMS 507		RP SEQUENCE FROM N.A.
Qy	514 VRDCAMLRRSPGPGVPAEFLRRLAEFLAKLHWLMSVYVVELLSFYYTETTQQRNL 573		RX MEDLINE=98241176; PubMed=9582020;
Db	508 VQDCRMARSSPENNVCVAEIRTRERLIAVFLFWLMDAYYELLESFYYTETTQQRNL 567		RA Greenberg R.A., Alisoppo R.C., Chin L., Morin G.B., DePinho R.A.;
Qy	574 FFYRKFSWKLQSOISGIRQHKLKVOLRELSEAEVROHREARPALLTSRSLRFPKPDGLRPI 633		RT "Expression of mouse telomerase reverse transcriptase during development, differentiation and proliferation.";
Db	568 FFYRKFSMWRQLQSOISGIVRHHLERVLQDLSQEBVRQEQANFAMPICRRLFPKPSGLRPI 627		RL Oncogene 16:1723-1730(1998).
Qy	634 VNMDTYVGFARFRERKAERLTSRVKALFSLVNEYBARRPGLIGSVLGLDDIHRWRTF 693		RN [2]
Db	628 VNMSY-MGTRAFDKGKQAOHQFTQCLKLTFSYVNLTKHTNLLGASVLGLNDIVTRWTF 686		RP SEQUENCE FROM N.A.
Qy	694 VLVRVRAQDPPPELYFVWDVGTGAYDTPQDLTEVIASITK-PQNTYCVERYAVVQRAAH 752		RA Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.;
Db	687 VLVRVRAQDPPPELYFVWDVGTGAYDTPQDLTEVIASITK-PQNTYCVERYAVVQRAAH 746		RT "Expression of mouse telomerase catalytic subunit in embryos and adult tissues."
Qy	753 GHVRKAFKSHYSTLTDLOPYMRFQYAHQ--ETSPSLRDAYVIEQOSSLNEAASSGLFDVFL 810		RL Proc. Natl. Acad. Sci. U.S.A. 95:10471-10476 (1998).
Db	747 GQIKHKSFRQVSTLSDQDQHNGQFLXKLDQSDTSALRNVSIVEQSLSNRASSSLDFFL 806		RN [3]
Qy	811 RFMCHHAVRTIGKSYTCOGCGPQGSLSITLCSLCYGMENKLFAIGTRGCLLRLYDDF 870		RP SEQUENCE OF 550-616 FROM N.A.
Db	807 RFVRNSVKGRCYQCGQGIPQGSLSITLCSLCYGMENKLFAEVQDGLLRLRFYDDF 866		RA Drissi R., Cleveland J.L.;
			RT "Parrial sequence of Mus musculus telomerase catalytic subunit homolog."
			RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
			CC FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for the replication of chromosome termini in most eukaryotes. It elongates telomeres. It is a reverse transcriptase that adds simple sequence repeats to chromosome ends by copying a template sequence within the RNA component of the enzyme.
			CC - SUBUNIT: Component of the telomerase ribonucleoprotein complex at least composed of TP1, EST1, EST1A, POT1 and a telomerase RNA template component (TER). Interacts with PIMX1 (By similarity).
			CC - SUBCELLULAR LOCATION: Nuclear.
			CC - SIMILARITY: Belongs to the reverse transcriptase family.
			CC This Swiss-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>

CC	or send an email to license@isb-sib.ch).	Db	753 QVTTLSDIQLQPMQFLKHLQDSASALRNSVYIEQSISMNESSSSLFDFFLFLRHSVVK 812
CC	EMBL; AR051911; AAC09333.1; -.	Oy	820 TREGKYYVOCOGTIPQGSTLSTLICSLCYGDMENKLFAIGIRRGILLRLYDDFLFLVTPHLTH 879
DR	EMBL; AF073311; AAC34821.1; -.	Db	813 IGDRCytcQGTGQSSLTLSCFGDMENKLFAEVQDGLLRFVDDFLFLVTPHLHQ 872
DR	EMBL; AF029235; ABB84200.1; -.	Qy	880 AKTFELRTLVRYGPBYGCVNLRKTVNNPVEDEALGCTAFVMPAHGLFPWCGSLLLDRT 939
MGBJ	MGI_11202709; Tert.	Db	873 AKTFELSTLVHGPBYGCVNLRQTVNNPVEPTGLGAAPYQPAHCLFPWCGSLLDRTQ 932
DR	InterPro; IPR000477; Rvse.	Qy	873 AKTFELSTLVHGPBYGCVNLRQTVNNPVEPTGLGAAPYQPAHCLFPWCGSLLDRTQ 932
DR	InterPro; IPR003515; Telomerase_RT.	Db	873 AKTFELSTLVHGPBYGCVNLRQTVNNPVEPTGLGAAPYQPAHCLFPWCGSLLDRTQ 932
DR	Pfam; PF0078; Rvt; 1.	Qy	940 LEVQDSSYARTSISRALSTLNFGKGAGRNMKLFGYURLKCHSLFQDLOQNSLQTVC 939
DR	PRINTS; PRO1365; TELOMERAERT.	Db	993 NIYKILFQAYRPHACVQLPFQRVRKNLTFLGISSQASCYAIKVNPGMTIKAS 1052
KW	DNA-binding; Nuclear protein; Ribonucleoprotein;	Qy	1000 NIYKILFQAYRPHACVQLPFQHQQWNKPTFFLRVTSATSLCYSILKAKNAGMSLGAK 1059
KW	DNA-directed; DNA polymerase; Telomerase; Transferase.	Db	993 NIYKILFQAYRPHACVQLPFQRVRKNLTFLGISSQASCYAIKVNPGMTIKAS 1052
FT	CONFLICT 553 I-> V (in Ref. 3)	Qy	1053 GS--FPPEAAHWHLYCYQFLKLAAHSTYKCLGPRTAQKULCRKLPPEATMTIKAA 1109
SQ	SEQUENCE 1122 AA; 127977 MW; F85266905DD6558C CRC64;	Db	1120 NPALPSDFKTILD 1132
Query Match	58.8%; Score 3505; DB 1; Length 1122;	Db	1110 DPALISTDFQTILD 1122
Best Local Similarity	64.4%; Pred. No. 2-2e-210;	RESULT 7	
Matches	719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;	Q9UBR6	PRELIMINARY;
Db	1 MTRAPRCRAVRSLSRSHREVLPLATEVRLGPQGWRLLVQRGDPAAFLVALVAQCLVCPW 60	ID	PRT; 524 AA.
Qy	1 MTRAPRCRAVRSLSRSHREVLPLATEVRLGPQGWRLLVQRGDPAAFLVALVAQCLVCPW 60	AC	Q9UBR6;
Db	1 MTRAPRCRAVRSLSRSHREVLPLATEVRLGPQGWRLLVQRGDPAAFLVALVAQCLVCPW 60	DT	01-MAY-2000 (TrEMBLrel. 13, Created)
Qy	61 DARPPAAPSFRQVSCLKELVARYLQLRCERGAQNLVLAFCGPPAFTTSVR 120	DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Db	61 GSQPDPADLSFHQVSSLKELVARYLQLRCERGAQNLVLAFCGPPAFTTSVR 120	DE	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Qy	121 SYLNTVTDALRGSGAWGILLRRGGDIDVYLHLLARCAEVLVAPSACAVQCGPLYQGA 180	GN	Name=TEXT;
Db	121 SYLNTVTDALRGSGAWGILLRRGGDIDVYLHLLARCAEVLVAPSACAVQCGPLYQGA 180	OS	Homo sapiens (Human).
Qy	181 ATQARPPPHAS-GPERRLG-----CERAMNEVSREVEAGVPLGQLPAPARRGGSARS 231	OC	Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi; Homo. Homo sapiens (Human).
Db	181 TTDIWPSVSSSYRPRPGRNFNTIRELQIKSSSRQEAQPKPLALPSGTKRLSLLTS 240	OC	Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo.
Qy	232 LPLPKRPRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVSPAR----PAEATTSLE 286	OX	[1] _TaxID=3606;
Db	241 VPSAKKARCYPVPRVEEGP-----HRQVLPPTSGKSM--VPSPARSPPEVTAERDSSK 292	RP	SEQUENCE FROM N.A.
Qy	287 GALGSTRSHPSVGROHHAGGPSTSRPRPWPDTCPCPVYAAETKHFLYSSGD-KEQLRSF 345	Q9UBR6	PubMed=10022128;
Db	293 GKVDPLSLSGVSCCKHKPSSTSLLSPRONAFOLQRFLIETRFLFLYRGDGQERLNPSF 350	RX	RA MEDLINE=99144726; PubMed=10022128;
Qy	346 LLSLRPSTLTGARRIVETFLGSRPMMPGTPRRLPRLPORYWONRPLFLELLGNHAQSPY 405	RA	RA Greenberg R.A., O'Hagan R.C., Deng H., Xiao Q., Hann S.R., Adams R.R., Lightsteiner S., Chin L., Morin G.B., Depinho R.A.;
Db	351 LLNSIOPNLTGARRIVEFLGSRPMMPGTPRRLPRLPORYWONRPLFLELLGNHAQSPY 410	RT	RT "Telomerase reverse transcriptase gene is a direct target of c-Myc but is not functionally equivalent in cellular transformation.";
Qy	406 GVLLKTHCPLRAA---VTPAAGVCAREKPGSVAAPEEEDTDPRRLVQLLQRHSSPQVY 462	RL	RL Oncogene 18:1219-1226(1999).
Db	411 VRLLSRSHCRPTANQVTDAL-----NTSPSPHMLDLRLHSSPQVY 452	RN	RN [12]
Qy	463 GFVRACLRRVPPGIGWSRHNEREFLRNTKKFKISIGKHAKLSQLQELTMKMSYRDCAWRR 522	RX	RP SEQUENCE FROM N.A.
Db	453 GFLRACKVVSASLWGTNRHNEREFLRNTKKFKISIGKHAKLSQLQELTMKMSYRDCAWRR 512	RA	RA WU K.J., Grandori C., Amacker M., Simon-Vermot N., Polack A., Lingner J., Dalla-Favera R.;
Qy	523 SPGVGCPAHEHRREELIAKFLHLWMSVYVELLRSFVXTETTFCQNLFFYRKSTWS 582	RA	RA Submitted (DB-1998) to the EMBL/GenBank/DBJ databases.
Db	513 SPGKDPRVAAEHLRERELATFLFMLMDTYVQLRSFVYTTESTFCQNLFFYRKSTWS 572	RN	RA SEQUENCE FROM N.A.
Qy	583 KLOSIGIROHLKRVOLRELSEAEYRQHREARPALLTSRFLPKDGLRPIVNNMDVYGA 642	RA	RA Szutorisz H., Palmquist R., Roos G., Stenling R., Schorderet D., Riedel R., Lingner J., Nabholz M.;
Do	573 KLQSQDQHOFHTORLTKTSMLNAYERTKPHMGSSVQMDYTRTFRAVFLVRVRLDQ 632	RL	RA Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
Qy	643 RTFREKRERLTSRKVAFPSVLYERARRPGJLGAStVGLDDIHRATFTFLVRLVRADP 702	DR	DR AF114847; ADD4164.1; -.
Db	633 RALGRKQAOHFHTORLTKTSMLNAYERTKPHMGSSVQMDYTRTFRAVFLVRVRLDQ 632	DR	DR AF114847; ADD4164.1; -.
Qy	703 PPELYFKVYDVTGAYDTIPDRLTEVIASTIK-PONTYCYRRAVQKAHGHRKAKS 761	DR	DR GO: GO_0003364; F:RNA-directed DNA polymerase activity; IEA. KW RNA-directed DNA polymerase.
Db	693 TPRMYFVKADEVGDAYAIPQGKLYEVVANNMRHSESTYCTROZAVRDRSDQGVHKSSRR 752	FT	FT NON TER 524
Qy	762 HVSTLTDIQLQPMRQPAHQBET--SPLRDAAVIBOSSLINEASAGLFFYFLRMCHHAYR 819	SQ	SQ SEQUENCE 524 AA; 57932 NW; 5F47DBFD01832B1B CRC64;
Query	Match 47.4%; Score 2825; DB 2; Length 524;		
Best Local Similarity	100.0%; Pred. No. 2.8e-168;		

Matches	Conservative	0	Mismatches	0	Indels	0	Gaps	0
Qy	1	MPPAPCRRAVSLRSHYREVPLPLATFVRLLGPGWRLVYORGDPAAFRALVAQCLCVWP	60					
Db	1	MPPAPCRRAVSLRSHYREVPLPLATFVRLLGPGWRLVYORGDPAAFRALVAQCLCVWP	60	Qy				
Db	61	DARPPAPPSFROVSLKELVARVLQRCEGAKNVLAFGPALLDGAGCAGPPAFTTSVR	120					
Db	61	DARPPAPPSFROVSLKELVARVLQRCEGAKNVLAFGPALLDGAGCAGPPAFTTSVR	120	Qy	186	PPP	--HAS--	-GPRRLIGCERAWNHSREAGVPLGLPAPGARRGGSSR-
Db	121	SVLNPNTTDALRGSGANCLLRLRVGDDVYLHLLARCAFLVLPASCAYQVCGPPLYQJGA	180					
Db	121	SVLNPNTTDALRGSGANCLLRLRVGDDVYLHLLARCAFLVLPASCAYQVCGPPLYQJGA	180	Qy	204	PSPGFVRRYSRFKNSLSDYVWKRCRP	--HYTLKSQWKRCRP	--RRGRVSSRR
Db	231							
Db	231							
Db	257	KRRSHRIQSLSRGYOPSAKYNFOAQGRIQISTVTALEKQCSSSLCPARAPSLSKRKRDGE	316					
Db	244	PE	--	--	-PRETPVGG-	--SW-	--	256
Db	244							
Db	317	VEITAKRVKIMEKEIHEQACIVD						
Db	257	--AHPR-	--	--TRG-	--	--		264
Db	374	NSEMSGPSVTHRSHPKRPYADKSSPPQGVQGNKRKTGTGABKRBNSNRRGLEMYINDIHK	433					
Db	265	PSDRGF-CVUSPARAE	--	--EATSI	LEGALSGTRSHPSVGROHHAGPPSTSRRPPRWDT	319		
Db	434	PNRRTERRINPTHKPELNSVOTEPMEGASSGDRKOE	--	--NPAHLAKOJPNNTL	4.84			
Db	301	ROPHAGPSTSREPRPMDTPCPVYAEETKFLYSSGDKEQLRPSFLSSRPSLTGARRL	360	Qy				
Db	301	ROPHAGPSTSREPRPMDTPCPVYAEETKFLYSSGDKEQLRPSFLSSRPSLTGARRL	360	Db	320	PCPPVYAEETKFLYSSGDKEQLRPSFLSSRPSLTGARRLVTETFLGSRPW	--M	372
Db	241	GAAPERTPVGGSWAHPGTRGPDSRGCFVYSPARAEATSLEGALSGTRSHPSVG	300	Qy				
Db	241	GAAPERTPVGGSWAHPGTRGPDSRGCFVYSPARAEATSLEGALSGTRSHPSVG	300	Db	485	SRSTTYFEKKFLSRYPKFSLSPQGCQGGRJETTFLISONQLIKEQQNQL	544	
Db	361	VETIFLGSRPMWGTTPRPLPQRYNMRPLPLELIGNHACQCPYGVLLKTHCPLRAAVT	420	Qy				
Db	361	VETIFLGSRPMWGTTPRPLPQRYNMRPLPLELIGNHACQCPYGVLLKTHCPLRAAVT	420	Db	373	PGTPTPRPLPRLPQYMQMRPLPLELIGNHACQCPYGVLLKTHCP	--LRAA	418
Db	421	PAAGVCAREKPQGSVALPPEEEDTPRLLVQLDQHSSPWQVQYFVRACLRLVPPGLMG	480	Qy				
Db	421	PAAGVCAREKPQGSVALPPEEEDTPRLLVQLDQHSSPWQVQYFVRACLRLVPPGLMG	480	Db	545	PQQKWRKRLPKRYQMRIFQKLVYHNEKCPYLVLRLRNCPVLLSACBLKKTTELTLQQA	604	
Db	481	RHNERFLRNTTKRKFISLGKHAKLSQELTWKMSVRDCAWLRRSP	524	Qy				
Db	481	RHNERFLRNTTKRKFISLGKHAKLSQELTWKMSVRDCAWLRRSP	524	Qy	419	VTPRAGV--CAREPKQG	--SVA--PEE	--EDTDPPRILVQLRQ
Db	605	605	LPGEAKVHKHTGEKGESTCTAPNSFLAPPSVLACQPERGEQHPPAEQSDP-LLRETEILRQ	663				
Db	455	HSSPMQVQYGVPRACDRLLPPGLWSRHNRERFLANTKPFISLGKHAKLSQELTWKMSV	514	Qy				
Db	664	HSSHMQVQYGVRECLEPVIKAELMSHNCICRFKVKAFISMGKXAKLSQELTWKMSV	723	Db	515	RDCAWLRLRSPGVCPAAEHRLLRELLTAKPLHMLMSVYVLLRSFFYVTTTFOQNRL	574	
Db	724	724	724 NDCWLRLAKGNHSPVAYEICYRETLAKFLYWLMSVYELLKSPSYITTMQDNMLF	783				
Db	575	FYRKSWSKLQSIGTRQHAKVQLRPELSEAEPHQHEARPALITSLRERIKPDGJRPPIV	634	Qy				
Db	784	784 YYRKPIWGLQNIQGRDHFAKVHLFALSSEEMEVTRQKCYPIASLRFIPNGNGLRPVV	843	Db				
Db	635	635 NMDYVVGARPF--RREKRAERLTSRKALESVLAYERAREPGLLGASVLGIDDIHRAWR	691	Qy				
Db	844	844 RLSRVUEGQKLSKESREKKIQRVNTQKJNFSVLYNVERTNTSILOSSVFRDDIRKWK	903	Db				
Db	692	692 TFEVLRV-RAQDPPEPPFLYVKVDYTFDGTAYDTIPLDRLTEVATSIKPF-QNTYCVRVAVVQ	748	Qy				
Db	904	904 EFTVKFESGEMPFYFQGDVSZAFDTIPHCKLVEVISOLVLPKPSQTVYGIRWAVIM	963	Db				
Db	749	749 KAANGHVRKAFKSHUSTLTDQPMNRQVAVLQESTPLRDAVVIESSSLNEASSGLFDV	808	Qy				
Db	964	964 ITPTGKARYKRVSTSFEDIPDNKQFVKSLQBERTSLRNAIVVECLTFNENSTLFTF	1023	Db				
Db	809	809 FLRFNCHHAVRIGKSYVQCGIPOSISLTLLCSLCYGMENKLPGIREDGLLRLVLD	868	Qy				
Db	1024	1024 FLCMLHNNLBIGHRYIYQSGIPQGSSILSTLLCSLCYGMENKLQGDLVRLRLLID	1083					
Db	159	Best Local Similarity	44.1%	Score	2590;	DB 2;	Length	1346;
Db	159	Conservative	44.1%;	Pred.	No. 4	5e-155;	Indels	242;
Db	159	Mismatches	350;	Gaps	29;			
Db	9	A VRSLLSHYREVPLPLATFVRLL-GPGCWRLVYORGDPAAFRALVAQCLCVWDARPP	65	Qy				
Db	25	AVLGALRGCYAEXTPLAEFVRRIQEGGTGEVELRGDDAACRTFVSCVVCYPRGRARAI	84	Db				
Db	66	PAAPSPFQVSLKELVARVLQRCEGAKNVLAFGPALLDGARGGPPPEAFTTSVRSLPN	125	Qy				

Db	1143	SWCGLLDIDVOTLEVVCDYSSAYAFTSIRSSLSFNSSRIAGKMKCKLTAVIILKCHPLILD	1202	320 PCPPVYAEKHFPLYSSGDKBQLRSPFLSSLRPSSLTKPQFLLTQARLVEVTFLGSRPW-----M 372
Qy	989	LOVNSLOTCTNIVKILLQAYRFACVLQPFHQOQWKPTFEVRISDTASLCYSTIK	1048	485 SRSTVYFEKKFLYRSYQEYFPFSFLSLRQCOAGGRBLIEITFLSQNPLKEQQNQL 544
Db	1203	LKINSQTVINIYKIFLQAYRFACVLQPFNQKVNPDFFLRISDTASCCYFLK	1262	373 PGTPRLPLPQRYWQMRPLFLEIIGNHACCPYGYLKTHCP-----LRAA 418
Qy	1049	AKNAGNSLGLARGAAAGPLPSAVQNLCHOAFLKLTRHRYTVVPLGSIARTAQTOQLSRKLP	1108	545 PQQKWRKRLPKRWTQMREFOQLYKHNHECPYLVRKNCPVLLSEACURKTELTQAA 604
Db	1263	AKNPGVSLGSKDAASGMFPFFAELCYHAFLVULSNHKVYKPLKVKYKMLFGKIP	1322	419 VTPAAGV-----CAREKPG-----SVAA-----PEE-----EDTDPRRLVQLLRQ 454
Qy	1109	GTTLTAAANPAPALPSDFKTLID 1132		605 LPGEAKVHKGHTERKESTEGTAPNSFLAPPSSVLAQGPGRGEOHPAEGSDP-LIRELLRQ 663
Db	1323	RDTMELLKTYTEPSLICQDPFTKILD 1346		
RESULT 9				
AAST5793		PRELIMINARY;		455 HSSPQWQVGFVRACLRLVPPGLMSVYVYELLRSFXYVETTFQKRNLF 574
AC	AAST5793	PRT;	1346 AA.	485 SRSTVYFEKKFLYRSYQEYFPFSFLSLRQCOAGGRBLIEITFLSQNPLKEQQNQL 544
DT	31-MAR-2004	(TREMBREL. 27, Created)		724 NDCTWLRLXKGNTNSVPAEHCYREBILAXFLYWMDSVIELRSFSFYTETMFQKNMLP 783
DT	31-MAR-2004	(TREMBREL. 27, Last sequence update)		575 FYRKSWWSKLOSSIGTIRKHLKRYVOLRELSAEVVRHREARPALLTSRLRFPDKGLRPIV 634
DT	31-MAR-2004	(TREMBREL. 27, Last annotation update)		784 YYRKEFWGLQNCIRDIFAKVHRLASEEMEVTRQCKYFPAASRLRTPKNGLRPVY 843
DE				
GN				
OS				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			635 NMDDYVGARTF--REKRAERLTSRKALFSVLYNERYARRPGILGASVGLDDIHRRAWR 691
OC	Archobacteria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			724 NDCTWLRLXKGNTNSVPAEHCYREBILAXFLYWMDSVIELRSFSFYTETMFQKNMLP 783
OC	Galii; Gallus gallus.			844 RLRSRVVEGGKLSKESREKIQNYNTQKLNFSLVNYERTVNTSIGSSVGRDDIYRKIK 903
OX				
RN				
RP				
SEQUENCE FROM N.A.				
RA	Delany M. E., Daniels L. M.			
RL	Submitted (DBC-2003) to the EMBL/GenBank/DBJ databases.			
DR	AY502522; AAS7573.1; -.			
KW	RNA-directed DNA polymerase.			
SQ	SEQUENCE 1346 AA; 15531 MW; E934B864FB6A4D40 CRC64;			
Query Match	43.4%; Score 2590; DB 2;	Length 1346;		692 TFLYRV-FQDQPPPELYFVFKDVTGAYDTIPODRLTEVIASTIKP--ONTCYCRRAYVQ 748
Best Local Similarity	44.1%; Pred. No. 4-56-153;			724 NDCTWLRLXKGNTNSVPAEHCYREBILAXFLYWMDSVIELRSFSFYTETMFQKNMLP 783
Matches	593; Conservative 159; Mismatches 350;	Indels 242; Gaps 29;		844 RLRSRVVEGGKLSKESREKIQNYNTQKLNFSLVNYERTVNTSIGSSVGRDDIYRKIK 903
Qy	9 AVPSLIRSHREVLPLAFLVRRRL -GPOGWLVRQGDA-AFFALVACCLVCPWDARPP	65		692 TFLYRV-FQDQPPPELYFVFKDVTGAYDTIPODRLTEVIASTIKP--ONTCYCRRAYVQ 748
Db	25 AVLGALRGCYAEXTPLEAFVRRQEGGTGEVEVLRGDDAQCYRTFVSQCVVCYPRGRAI	84		724 NDCTWLRLXKGNTNSVPAEHCYREBILAXFLYWMDSVIELRSFSFYTETMFQKNMLP 783
Qy	66 PAAPSFROVSCLKELVARVLQRUCERGAKNVAFLGFAALDGARGGGPEAFTSVRSYTLPN	125		844 RLRSRVVEGGKLSKESREKIQNYNTQKLNFSLVNYERTVNTSIGSSVGRDDIYRKIK 903
Db	95 PRDIFCQQLSQSEDEVTRIVQRLCEKKNNLAYGYSILDEUSCHPFLVPLSSISTLN	144		692 TFLYRV-FQDQPPPELYFVFKDVTGAYDTIPODRLTEVIASTIKP--ONTCYCRRAYVQ 748
Qy	126 TYTDALRGSGANGUILLRRVGDYLVHLARCALFVLYAPSCAYQVCPPLYQLGAAATQAR	185		724 NDCTWLRLXKGNTNSVPAEHCYREBILAXFLYWMDSVIELRSFSFYTETMFQKNMLP 783
Db	145 TVTEITRISGLWILLSLRIGDDYMMYLHECAFLPMVPSNCYQCCQIVYL-ISRNVG	203		844 RLRSRVVEGGKLSKESREKIQNYNTQKLNFSLVNYERTVNTSIGSSVGRDDIYRKIK 903
Qy	186 PPP-----HAS--GPRRLGGERBANNHSVEAGVPGIPLPAGARERGGSAASR-	230		692 TFLYRV-FQDQPPPELYFVFKDVTGAYDTIPODRLTEVIASTIKP--ONTCYCRRAYVQ 748
Db	204 PSFGFVRRYYSRFKHNSTLDYTRKLYFHR--HYLSKSQWIKCRP---ARRGRYSSR	256		724 NDCTWLRLXKGNTNSVPAEHCYREBILAXFLYWMDSVIELRSFSFYTETMFQKNMLP 783
Qy	231 -----SLPLP-----SLPLP-----KRPRRGAA 243			844 RLRSRVVEGGKLSKESREKIQNYNTQKLNFSLVNYERTVNTSIGSSVGRDDIYRKIK 903
Db	257 KRRSHR1QSLRGYQPSAKVNQAGRQ1STVARTLERQKSCSSLPARAPSLRKRDGEQ	316		692 TFLYRV-FQDQPPPELYFVFKDVTGAYDTIPODRLTEVIASTIKP--ONTCYCRRAYVQ 748
Qy	244 PE-----PERTPVGGQ-----SN-----	256	RESULT 10	
Db	317 VEITAOKVIMKKEIEQACSTIVPD---VNQSSSSQRHGTSWHVAPAVGLIKEHYISERS	373	Q9DE32 PRELIMINARY;	
Qy	257 -----AHPCR-----	264	Q9DE32 PRELIMINARY;	
Db	374 NSEMMSGPSVVRSHPGKRPVADKSSFFQGVQGNKRKTKGAEKRAESNRGLEMVINKH	433	AC Q9DE32 PRELIMINARY;	
Qy	265 PSDRGF-CVVSPPARPAE---EATSLEGALSTRHSHPSVRQHHAGPPSTSRRPRPWDT	319	AC Q9DE32 PRELIMINARY;	
Db	434 PWRGGLERRINTTHKPLNSVQTEPMEGASCDRKQF-----NPAPLAKQPLNT	484	AC Q9DE32 PRELIMINARY;	
Qy			01-MAR-2001 (T-EMBLrel. 16, Created)	
Db			01-OCT-2003 (T-EMBLrel. 25, Last sequence update)	
Qy			01-OCT-2003 (T-EMBLrel. 25, Last annotation update)	
Db			Telomerase reverse transcriptase.	
GN	Name=BERT;			
OS	Xenopus laevis (African clawed frog); Metaoza; Chordata; Craniata; Mesobatrachia; Pinimidae; Eukaryota; Batrachia; Anura; Mesobatrachia; Pinimidae; Bivalvia; Eumetazoa; Bilateria; Euteleostomi; Amphibia; Amphi;			
OC				

OC	Xenopodinae; Xenopus.	Db	632 RKSVMKKLQNLGKHLERYKLRSUSSDELENMQMKNVPLVSURFPIKNGLRPISKI 691
RN	[1] NCBI_TaxID:8355;	Qy	637 DYVVGARTFR--REGRAERIUTSRVRALEFSVLYTEARRPGILGASTVLGLDDIHRARWRTFV 694
RP	SEQUENCE FROM N.A. PubMed-11602347; MEDLINE=2148834;	Db	692 SSTLSQQSENQERKHHFSSQRNLFSVLYENRNCSLIGGSFGMDDIYCKWKFV 751
RA	Kuranoto M., Ohsumi K., Kishimoto T., Ishikawa F.; "Identification and analyses of the Xenopus TERT gene that encodes the catalytic subunit of telomerase." Gene 277:101-110 (2001)	Qy	695 LRV-RAQDPPEPELYFVKDVTGAYDTIPQDRLTETIASIKP-QNTYCVRAYVQKAA 751
RT	RL EMBL-AF212299; AA[GAT]3537.1; -;	Db	696   :
RT	DR CO; GO:0005634; C:nucleus; IEA.	Qy	752 LDFERPQVBKLQFYFVKTDYKGATDTIPHSKLDEVTSKVYINPNANEVYIRRATYVSVPD 811
RT	DR GO; GO:0003677; P:DNA binding; IEA.	Db	753 HGHTRKAFKSHVSTLTDQYIMRQEVHLOETSPURDAVVEQSSSLNEASSGLLPDVFLR 811
RT	DR GO; GO:0003723; P:RNA binding; IEA.	Qy	812 TGRIIKSFRKHVSLEADVLPMKQTVSNQOEKRNLRLNTLIVEQNLLNESSVKLLAVFQQ 871
RT	DR GO; GO:0003964; P:RNA-directed DNA polymerase activity; IEA.	Db	812 FMCHAVRARGKSYQCOGIPQGSILSTLICSLCYGDMDMENKLPGAFTRRDGILLRLYDDFL 871
RT	DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.	Qy	872 IIRSHLRLKDRYMQCCGIPQGSILSTLICSLCYGDMDENAMLGJQKNEVLMRLIDDFL 931
RT	DR InterPro; IPR003545; Telomerase_RT.	Db	872 LYTPHILTHAKTFLRTLTVRGYPEYGCYVNLRKTVNFPVFD - EALGGTAVQMPAHGLFP 929
RT	DR Pfam; PF00078; RVT; 2.	Qy	932 LVTPHILDOAKTFLRTLAEGLPQYQGCSISPORTVNNFPVVDIPEC -- SEYEQLPHCLFR 988
RT	DR RNA-directed DNA polymerase; Transferases.	Db	932 WCGLLLDOTRPLEQEDYYSSYARTSTRASLTFENRQPKAGRMRRKLFGVURLKCSLFLDL 989
RT	SW SEQUENCE 1191 AA; 138016 MW; 9BD9D77686A57D6 CRC64;	Qy	989 WCGLLLDOTQDLYDYSSYACTSISTRSMTPFCHSSAAGKYMQKOKLIRVLRKCSLFLDL 1048
Best Local Similarity 38.9%; Score 2316.5; DB 2; Length 1191;	Db	990 QVNLSQTVCNTYKILLQOYRFRAVCVLOPFPHQOYWKNPTEFFRVISDASLYC SILKA 1049	
Matches 518; Conservative 201; Mismatches 381; Indels 123; Gaps 25;	Qy	1049 KVNSRTRVCNTYKILLQYRFRAVCVQLPFGQVVMNNPFELTVISDAPCPFTTFKA 1108	
Qy 1 MPRAPCRAYRSLLRSHREYVPLATFVRLG-PQGWR - LVQRGDPAAFRALVAQCLYC 57	Db	1050 KNAGMSLGAKGAAAGLPSEAVQWLNQHQAFLKLTRHRTVYVPLGLSLRITAQTOSRKLPG 1109	
Qy 1 MPLRTCGATLUSILQRLQYGVQLGIVETYDTIQVPGCIVKPVILLESDSEKERSFAELVYC 60	Qy	1109 KNKDLTRGYKDVDSQFCNFNEAVQWLNQYQAFLTKLHNHKVLYKCLISPLQNCMQLSRRLSQ 1168	
Qy 58 VPWDARPPAAPSFRQSVCLKEBLVARVLQRCERAIAKVNIAFGFALLDGARGGPPEAFTT 117	Db	1110 TTATALEAAANPALESDFKTLD 1132	
Qy 61 IPRGTKPLPSPVSEFOLQSTQREVAVIQRICECEKRKVNLAFCGLVDE-EKNSLNIRLTP 119	Qy	1169 DTBELLKSVTDDSSHLDKDFSCIMD 1191	
Qy 118 SVRSYLPTNTVDAORGSGAWCLLIRRGGDVTVLHJARCALFVLYAPSCAYQVCGPPLY-	Db	RESULT 11	
Qy 119 NICNFNPNTTTTISTSLMETLITRQDDMMYWLQCSIFVYPRCCYQIRGQPYT 176	094807 ID 094807 PRELIMINARY; PRTR; 523 AA.		
Db 120 NICNFNPNTTTTISTSLMETLITRQDDMMYWLQCSIFVYPRCCYQIRGQPYT 179	AC 094807; DT 01-MAY-1999 (TREMBLrel. 10, Created)		
Qy 117 -----QIGAAATOR----- PPHASGPRRLGGERAINTHSVRE 209	AC 094807; DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)		
Db 180 LPSSDDVFLFQSOSFTQSNVLLRYIKRNVFHLRKKYLKPKHSMITSRM-----LTWRRNKS 234	AC 094807; DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
Qy 210 AGVPUGLPAPEARRGGSARSRL-----PLPKRERGGAPE-----PERTPVGQG 254	DB Telemerase transcriptase (Fragment).		
Db 235 SGLLRSKTSMAVTTEIHSRKKLCSKDIICVTPDKRNDLKDDTVDHPDLPMCRSVSYL 294	GN Name=hTERT;		
Qy 255 SWAHPGR-----TRG-PSDRGFCVSPARPAEATSLSLEGALSGTRH-----	OS Homo sapiens (Human).		
Db 295 SNMYPKTNVQVGTGLTGYKTKTFOCQKESQCKTAFYSAVGDNCNLSLKDVNKLJ 354	OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. NCBI_TaxID=9606;		
Qy 295 SHPSVGRQHAGGPSTSRRPRWPDTCPCPYTAETKHFY-SGGDKEQLRPSFLSSLRPS 353	RN [1] _SEQUENCE FROM N.A.		
Db 355 TNASV-----PTAQSR-----LSFSNIFIDFGRTYLVLISYKGSSESFLNSLDST 401	RT MEDLINE=913784; PubMed=9973199;		
Qy 354 LTGARRLVETFLGS-----RPMPGTPRRLPRLPQXYWQMPLFLLELGNHQCPY 405	RA Takakura M., Kyo S., Kanaya T., Hirano H., Takeda J., Yutsubo M., RA Inoue M.; "Cloning of human telomerase catalytic subunit (hTERT) gene promoter and identification of proximal core promoter sequences essential for transcriptional activation in immortalized and cancer cells."; DR EMBL; AB016767; BAA14728-T-. FT NON_TER 523 523		
Db 402 PSGSQKLVEFLNSNLAEEQFDQPARDENRY-KLPKRYWKMKPHEQELIONHKKFY 459	SQ SEQUENCE 523 AA; 56555 MW; 8FD562DDEC93DA CRC64;		
Qy 406 GVLLKTHCPLRRAAVTPAGYCAREQPSVAAPEED-----TDPRLVQLLQRQHSS 457	Query Match 37.0%; Score 2207.5; DB 2; Length 523;		
Db 460 LVIYLNKHPVSSM-----ACSERK--SLSQRNRTENDGKQKHTTAKNLSSLKQHSS 511	Best Local Similarity 78.7%; Pred No. 1..1e-129;		
Qy 458 PWQNYGPRVACRLRLLVPGIWLGSRHNRNERRFARNTKPKISL-GKHAKLSSLQBLTWKMSVRD 516	Matches 435; Conservative 3; Mismatches 56; Indels 59; Gaps 6;		
Db 512 IWQVNMFRVRECLNNYPDIMWGSNSHNCRFRNTVSEFLFFSGKFKSISLSELMMSMRVED 571	1 MPAPRCRAYSLLRSHREYVPLATEFVRLGPQGMWLVORGDDPAAFRALVAQCLVCVPN 60		
Qy 517 CAWLRSRSPGVGCVPAABHRREBEILAKFLWHLMSYVVELRSFFYVETFQKNRLLFY 576	1 MPAPRCRAYSLLRSHREYVPLATEFVRLGPQGMWLVORGDDPAAFRALVAQCLVCVPN 60		
Db 572 CSWIRLQSKSDHFVPASEHLLREKILAKFVFLMDTYVQIQLKSFFYVETMFQKHLLFY 631	1 MPAPRCRAYSLLRSHREYVPLATEFVRLGPQGMWLVORGDDPAAFRALVAQCLVCVPN 60		
Qy 577 RKSVNSKLQSQGIROHLKRYQVRELSEAEVRQHREARPALLTSRURPKPDGLRPIVNM 636			

QY	61 DARPPPAAPSPFQVSCLEKELVARYIQLCPRGAKNVLAEGFALLDARGCGPPEAFTTSYR	120	DR PRINTS; PR01365; TELOMERASERT.
Db	61 DARPPPAAPSPFQVSCLEKELVARYIQLCPRGAKNVLAEGFALLDARGCGPPEAFTTSYR	120	KW RNA-directed DNA polymerase; Transferase.
QY	121 SYLPNTVTDAIRGSAGLILRRVGDVLVHLLARCALFVLVAPSACAYCQGPPLYQLGQ	180	FT NON-TER 1 1
Db	121 SYLPNTVTDAIRGSAGLILRRVGDVLVHLLARCALFVLVAPSACAYCQGPPLYQLGQ	180	SQ SEQUENCE 575 AA; 65672 MW; F80C81BD7F6M91A3 CRC64;
QY	181 ATQAPPFHGSPPRLGERCAWNHSREAGVPLGLPAGARRGGSAARSLLPKRPRR	240	Query Match 33.8%; Score 2016; DB 2; Length 575;
Db	181 ATQAPPFHGSPPRLGERCAWNHSREAGVPLGLPAGARRGGSAARSLLPKRPRR	240	Best Local Similarity 67.6%; Pred. No. 1..2e-117;
QY	241 GAAPPERTPYGQGSWAHPTRGRPSDRGICVUSPARAPEATSLLEGALSGTRSHSPVG	300	Matches 391; Conservative 71; Mismatches 110; Indels 6; Gaps 3;
Db	241 GAAPPERTPYGQGSWAHPTRGRPSDRGICVUSPARAPEATSLLEGALSGTRSHSPVG	300	Qy 558 RSPFVYTTETPQQRLEFFRKWSKLSQGIGTQHLKEVOLRESEAEVQHREARPALL 617
QY	301 RQHHAGPSPSTSRRPRPWDTCPVYTAETKHFLYSSGDKEQLRPSFLSSLRPLTGA	360	Db 1 RSPFVYTTETPQQRLEFFRKWSKLSQGIGTQHLKEVOLRESEAEVQHREARPALL 60
Db	301 RQHHAGPSPSTSRRPRPWDTCPVYTAETKHFLYSSGDKEQLRPSFLSSLRPLTGA	360	Qy 618 TSRURFIPKPDGURPIVNDYVIVGARTFREKRAERLSRVKALFSVNLYERARPGLG 677
QY	361 VETIFLGSRWMPGPTRPLPQRYWONRPLFELIGNHAQCPYGVLIKTHCPLRAAVT	420	Db 61 ICRLRFIPKPNGLPIVMSYSNGCTRAGRKQQHQHFTQLRKTFSMLNYERTPHPLMG 120
Db	361 VETIFLGSRWMPGPTRPLPQRYWONRPLFELIGNHAQCPYGVLIKTHCPLRAAVT	420	Qy 678 ASVILGDDIHRAWTTFVLRVRAODPPPELYFVVKDVTGAYDTIFQDRLTIEVIASIIK-FQ 736
QY	421 PAAGYCAREKPQSYVAAPEEBDTDPRLVQOLLRHSSPQVYGVTRACURRLVPPGLW-	478	Db 121 SSVLMNDIYRTWAFVLRVRAUQFVQXAVVAMIRHSE 180
Db	415 -----CELRSPQQPVSP-----GRSPRAL-----W-----RPPRRTQTPVANCS	450	Qy 737 NTVCYRRVAVVOKAHHGHYRKAFKSHVSYSTLTDLOQYMRQFVAHQET--SPRLDAVVEQ 794
QY	479 -----GSHHNERRFLRNTKKFISLGKHAKLSQLELTWK 511	511	Db 181 STCYTQAVVRISOSQGHKSPTROVTTLSDQDSALRSRNVSWEQ 240
Db	451 CSASTAPLAGVRLRAGLAPAGAPRPLGQAQRRLFLRNTKKFISLGKHAKLSQLELTWK	510	Qy 795 SSILINEASSGLFDVLFRENCHHAIRIGKSYVOQGIPGCGSISLTLSCLGMDMENKL 854
QY	512 MSVRDCAWLRSP 524	524	Db 241 SISNESSSSLFDFELHLRHSVVKIGRCYTCQCGIQGSSSLSTLSCLGMDMENKL 300
Db	511 MSVRDCAWLRSP 523	523	Qy 855 AGIRRGILLRLYDDFLLVTPHLTHAKTFFLRLTVRGPEBGCVNLRKTUVNPVEDBAL 914
QY	RESULT 1.2		Db 301 AEVQDGILLRFVDLFLVTPHLDQAKTFLSTLHVGPBYGCMNLQKTVNFPVEPGL 360
Q9JTK9	PRELIMINARY; PRT; 575 AA.		Qy 915 GGTPFVOMPAHGLFPWCGSLLDPITLQEYDSDYSSYARSTISIRASLTENGEKAGRMREKL 974
AC	Q9JTK9;		Db 361 GGAPAPQLPAPHCLFPWCGSLLDPITLQEYDSDYSSYARSTISIRASLTENGEKAGRMREKL 420
DT	01-OCT-2000 (TREMBrel. 15, Created)		Qy 975 FGVLRLKCHSLFLDQLQNSLQTCTNIVKILLQAYRPHACVQLPFIHQWIKPTFFLR 1034
DT	01-OCT-2000 (TREMBrel. 15, Last sequence update)		Db 421 LSVLRLKCHGLFELDQLQNSLQTCTNIVKIFLQAYRPHACVQLPFIHQWIKPTFFLR 480
DT	01-OCT-2003 (TREMBrel. 25, Last annotation update)		Qy 1035 VISPTASILCYSTILKAKNAGMSLGKGAQGPLSEAVQWLCHOAFLKLULTRHRYTYVPLG 1094
DE	Telomerase catalytic subunit (Fragment).		Db 481 IISQASCCYIILVKVNPGMTLKAAGS---FPPDAHMLCYQAFLLKLAHSVYKCLLG 537
OS	Ratetus norvegicus (Rat).		Qy 1095 SURTAQTQSLRKLFGTUTALEAANPALPSDFTKILD 1132
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		Db 538 PLRPAQKLCKRLFEATMTILKAADPALSTDQFTKILD 575
NCBI_TaxID	10116;		
RN	[1]		RESULT 1.3
RP	SEQUENCE FROM N.A.		Q9R266 PRELIMINARY; PRT; 514 AA.
RX	MEDLINE=22860253; PubMed=13679242;		ID Q9R266
RA	Wong S.C., Ong L.L., Er C.P., Gao S., Yu H., So J.B.; "Cloning of rat telomerase catalytic subunit functional domains, reconstitution of telomerase activity and enzymatic profile of pig and chicken tissues.";		AC Q9R266
RT	Life Sci. 73:2749-2760 (2003).		DT 01-MAY-2000 (TREMBrel. 13, Created)
RT	[2]		DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
RT	SEQUENCE FROM N.A.		DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)
RA	Wong S., Gao S., Xu X., Yu H.; Submitted: MAR-2000 to the EMBL/GenBank/DDBJ databases.		DE Telomerase reverse transcriptase (Fragment).
DR	EMBL; AF47818; AAF62177.1; -;		GN Name=Test;
DR	GO:0005634; C:nucleus; IEA.		OS Mus musculus (Mouse).
DR	GO:00003677; F:DNA binding; IEA.		OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.
DR	GO:00003723; F:RNA binding; IEA.		NCBI_TaxID=10090;
DR	GO:0003964; F:RNA-directed DNA polymerase activity; IEA.		RN SEQUENCE FROM N.A.
DR	GO:0003721; F:telomeric template RNA reverse transcriptas...		RX MEDLINE=9914726; PubMed=10022128;
DR	GO:00016710; F:transcriptase activity; IEA.		RA Greenberg R.A., O'Hagan R.C., Deng H., Xiao Q., Hann S.R., Adams R.R., Lightsciner S., Chin L., Morin G.B., Depinho R.A.,
DR	GO:0006228; P:RNA-dependent DNA replication; IEA.		RA "Telomerase reverse transcriptase gene is a direct target of c-Myc but is not functionally equivalent in cellular transformation.";
DR	InterPro; IPR000477; RVTse.		RT Oncogene 18:1219-1226 (1999).
DR	InterPro; IPR03545; Telomerase_RT.		DR AF121949; AAD24165.1;
DR	PFam; PF00078; RVT; 1.		DR GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

RNA-directed DNA polymerase.	GO: GO:0003677; F:DNA binding; IEA.
NON-TER	GO: GO:0003723; F:RNA binding; IEA.
SEQUENCE	GO: GO:0003954; F:RNA-directed DNA polymerase activity; IEA.
Best Local Similarity	GO: GO:0003723; F:telomeric template RNA reverse transcriptas. . . ; IEA.
Matches 304; Conservative 50; Mismatches 142; Indels 46; Gaps 10;	GO: GO:0003723; F:transerase activity; IEA.
1 MTRAPCRPAVSLRSRREVPLATEYVRRLGPQGWRLVQRGDPAFAFRALVAQCLVCYFW 60	GO: GO:0006279; P:RNA-dependent DNA replication; IEA.
61 DARPPPAFPFQVSCLELVARVLRQICERGAKNVLAFGPAFLDGAGGGPAAFTTSVR 120	InterPro: IPR00215; Proc_inh_serpin.
61 GSQQPAIDLPHQVSSLKELVARVLRQICERGAKNVLAFGPEKTYRTLVAQCLVCYFW 60	InterPro: IPR00477; RTse.
121 SLPNTVTDALRGSGAWGLLRRVGDDLVHLARCAFLVLPASCATYQCVGPPLYOLGA 180	PRINTS: PRO0354; TELOMERASE_RT.
121 SLPNTVTDALRGSGAWGLLRRVGDDLVHLARCAFLVLPASCATYQCVGPPLYOLGA 180	PROSITE: PS00284; TELOMERASE; Transerase.
181 ATQARPPPHAS-QPERRRLG-----CERAMNHVSREVAEGVPLGLPADGARRGGSSARS 231	KW RNA-directed DNA polymerase; Transerase.
181 TTDIWPVSASYSTRPGRNFTNLRLQIKSSSQQAPKPLAPLSGTKEHLSLTSTS 240	SEQUENCE 1123 AA; 13051 MW; 44F243295817B7F6 CRC64;
232 LPLPKRPRGAADEPERTPVQGGSWAHPGTRPSDRGFCVSPAR----PAEATASLE 286	Query Match 12.2%; Score 724.5%; DB 2; Length 1123;
Db 61 GSQQPAIDLPHQVSSLKELVARVLRQICERGAKNVLAFGPEKTYRTLVAQCLVCYFW 60	Best Local Similarity 23.9%; Pred. No. 1.6e-36;
Db 121 SLPNTVTDALRGSGAWGLLRRVGDDLVHLARCAFLVLPASCATYQCVGPPLYOLGA 180	Matches 29; Conservative 192; Mismatches 506; Indels 237; Gaps 39;
Db 181 TTDIWPVSASYSTRPGRNFTNLRLQIKSSSQQAPKPLAPLSGTKEHLSLTSTS 240	Query Match 1 MPRAPCRAVRSLRSRHYREVPLATEV-----RLGPQGWR-----L 38
Db 232 LPLPKRPRGAADEPERTPVQGGSWAHPGTRPSDRGFCVSPAR----PAEATASLE 286	Db 1 MPRKRHRVEILVRLFGARNLNDIAVLPINNIQPEQCRQRQGLGCSSD1KAFL 60
Db 241 VFSAKKARCPYPRVEGP----HRQVLPPSGKSW-VPPPARSPSPEVPTAEKDLSK 292	Query 39 VQRGDPAATRALVACQLCVCPWDAPPADSPFRQUSCLKELVARYLQLRQ---CERGAKN 95
Db 287 GALSGTRSHPSYGROHHAGPPSTSRRPWRDTPCPVVAETRHFLLYSGD-KEQLRPSF 345	Db 61 LRSDDPPIHYTKLHLRHFV-VLHEQTPLDFFSPTSWQSREIVERLIEMMQSGCD---CQN 117
Db 293 GKVDSLIS-GSTCCKHXPSPSTSLLSPRQNAQQLRP-FTEETHFLYRGDGBRLNPF 350	Query 96 VLAFGFALIDGARGGPEAFTTSYRSYLPNTVTDAIRGSGAWGLLRRVGDDLVHLARCA 155
Db 346 LISSLRPSLTGARRLVETIFLGSRRPMGGTQRLPRLQRYWMQMRPLFLLLGCHNAQCQY 405	Db 118 VICARDYDQG-----SPILLETT-SSSWEFLIKRVEGDVMVLLQQ 159
Db 351 LLSNLQPNLQMLTGAARRLVETIFLGSRRPTSGPLCTHRLLSRRYWQMRLFQQLJYNAEQQY 410	Db 156 CALFVLUVAPSCAYQVCGPPLYQLGAAT----QARPPPHASGPERRRLGGERAWNNSVRE 209
Db 406 GVLKHKCPLRIA--VTPAAGYCAREKPGQSYVAAPEBDTDPRLVOLLROHSSPWQY 462	Db 160 TSIFPLLGKHHQVSGPPACIKHHRRTLSVHENKRDNNQQPPTQWLSSAVDODPKD 219
Db 411 VRLLSHSICRTANQQTDAL-----NTSPPHMLDLRLHSSPNOVY 452	Query 210 AGVFLIGLPAFG---ARRPGGASATSLPLKDKRPPRGA-----AEPERPTPGQSQWA 257
Db 463 GFVFRACLRLRVPPGLWGSRHNERFLRNTKFKISLGKHAKLSQLELTWKMSYRDCANLRR 522	Db 220 DSATI-TPLVGEDVDQHREKKTKRSRIVLKKRQRKVNFKVDCNAPCITP-----271
Db 453 GFVFRACLCKVVSASLWGIRHNERFLRFFKNLKFKISLGKIGKSLQELMWKMKVVEDCHWLRS 512	Query 258 HPGTRGPSPDRGFCVVSPARPAEATSLLEGALSQTRSHPSVGRQHAGPPSTSRRPRPW 317
Db 523 SP 524	Db 272 -- STNGKYSTG-----NDENMLHIGINGSLTDFKQAKQ-----303
Db 513 SP 514	Query 318 DTPCPVVAETKHFLYS-SGDKEQLRPSFLSSLRPSLTGARRLYTFLGSRPWNPGTP 376
RESULT 14	Db 304 -----VCRNKNPXGGLSETSYTIPNHTLKTRNCSDSKLLMHNIFGIVNVNNTTPS 356
Q9SE99 ID Q9SE99 PRELIMINARY; PRT; 1123 AA.	Query 377 RRLPRLQ----RIVQMRPLFLELIGNHACQPGVYLKHTCP-----IRANVTPAAG 4.24
AC 09SE99; DT 01-MAY-2000 (TREMBLrel. 13, Created)	Db 357 HGKENCPCGSSICLYHSLLSLKNLIGKTSSHLKMLDKHCPVJLQEDALKSGTSQS 416
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	Query 425 VCAREK-----PGSVA-----PEEEDTDPRRLVQLLQRHSSPQWQYGFVRACLRLVPPG 476
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	Db 417 -RQQRADLPHGSSQQTGKPCPSVEKL-----CTNDQVTFNIVACRTVPE 468
DE Name=TBRT; DE Name=TBRT;	Query 477 LWGSRHNERFLRNTKFKISLGKHAKLSQLELTWKMSYRDCANLRRSPGVCVPALEHRL 53.6
GN Arabidopsis thaliana (Mouse-ear cress).	Db 469 LLGPTHQMLVQMLTAWFVSRRLNEKCTYQFLHKVKPSDFPFFAKE---LCCMYNGHEL 52.6
OS Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta;	Query 589 IROHLKRVOLRELSEAVRORHREARPALTSRLRPTPKPGLRPIVNMDDYVGARTFRRE 64.8
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.	Db 587 ISKAIDGYLVDDAEESRK-----ISKFRPLPKANGVRWLD-----FSSS 63.0
OX NCBI_TaxId=3702; [1]	Query 649 KRAERLTSRKVAKFSLVNEYERARRPGLGASVGLDIDHAWRFTVLRVRAQDPP-PELY 70.7
RN SEQUENCE FROM N.A.	Db 631 SRSRSTSTQMLCTKWMISWFLIEVYKLVHENFNTATESQGRNLNYYYRGWSWERLISKE 5.86
RC STRAIN_Landberg erecta;	DR 708 FVKDVTGAYDT1QDRLEFEVIASLKPONTYCVRVAQKAAGH-----VRAFKS 76.1
RC MEDLINE=20070956; Published=10611235;	RA Fitzgerald M.S., Riha K., Gao F., Ren S., McKnight T.D., Shifren D.E.;
RA "Disruption of the telomerase catalytic subunit gene from Arabidopsis inactivates telomerase and leads to a slow loss of telomeric DNA.",	DR 649 KRAERLTSRKVAKFSLVNEYERARRPGLGASVGLDIDHAWRFTVLRVRAQDPP-PELY 70.7
RL Proc. Natl. Acad. Sci. U.S.A. 96:14813-14818 (1999).	DB 631 SRSRSTSTQMLCTKWMISWFLIEVYKLVHENFNTATESQGRNLNYYYRGWSWERLISKE 5.86
DR EMBL; API172001; AND55271.1;	GO: GO:0005534; C:nucleus; IEA.
GO: GO:0005534; C:nucleus; IEA.	

DR	InterPro; IPR003515; Telomerase_RT.
DR	PRINTS; PR00078; RVT; 1.
DR	PRINTS; PRO1365; TELOMERASE_RT.
DR	PROSITE; PS0284; SERPIN; UNKNOWN_1.
KW	RNA-directed DNA polymerase; Transferase.
SEQUENCE	1123 AA; 130579 MW; 564588295817B7F6 CRC64;
SQ	
Query	Query Match 12.2%; Score 724.5; DB 2; Length 1123; Best Local Similarity 23.8%; Pred. No. 1.6e-36; Mismatches 199; Indels 233; Gaps 39;
Db	1 MPRAPRCAVRSLAIRSHREVLPLATEV-----RRIGPQWR-----L 38
Db	1 MPRKPRHRPEILWRLFGNRARNLNDAIVDLIPRNIOQQCRGQGLGCSSDKPAFL 60
Db	39 VQRDPDPAAPALVAQCLVCWPDARPPAAPSFRVSCLKELVLRQL--CEPGAKN 95
Db	61 LRSDDPPIHYRKLLHRCFV-VIHEOTPPLDFSPSTSWSQEIVIEMMNGSGCD -CQN 117
Db	96 VLAFGFALLDGARGGPPEAFFTSVRSYLPNTVTDALRGSGAWGLLURRVGDVLVYLARLL 155
Db	118 VICARYDKYDOS-----SPOILELT-SSSWEFLIKRQHDVWYTLQQ 159
Db	156 CANFVWABSCAQYQCGPPLYQZAAAT-----QARPBPHASGPRRLIGGERAVAHNSVRE 209
Db	160 TSITLPLJUGKKHQGSQPPCLCIKHKRKTSVHENKRKDNNVQPPTKROWLSSAVDCCPKD 219
Db	210 AGVPGLPLPAG -----ARRGGASAESSLPLPKPRGQA-----APEGPRTVGGSWA 257
Db	220 DSATI-TPIYGEDUDQHRRKKTTRSRVYIKRRKQKVKUNFKKVDCDNAPCITP-----271
Db	258 HPGRTGRGPDSRGFCVSVPARPAAEATSTLEGALGSTRHSHPSPVGROHAGPSTSRRPPRW 317
Db	272 ---STNGKVSTG-----NDENMLJIGINGSLTDFYKQAKO-----303
Db	318 DTCPDPPIYAKETKHYLS-SGDKEQLRPSFLSSLRPLTGARRLVEFTIFLGSRPMGPTP 376
Db	304 -----VCRNKNPKFGLSETSYVPPNHLTKLURPNCSDSKLJLMHIFGEVNWNSTTPS 356
Db	377 RLRLRPQ ---RYWQMRPLFLELIGNHACQCPYGVLKTHCP-----LRAAVTPAAG 424
Db	357 HGKGNCPGSSCITYHSLSKLNLGKTKSSHLKMLDTRCPVPLLQEDALKSGTSQSS 416
Db	425 VCAREK ---POGSVA ---PEBEDTDPERLYQOLRHOSPFWVQYGFVRACLRRLVPPG 476
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ID	Q9SPU7
AC	Q9SPU7_13; Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE	Telomerase reverse transcriptase.
GN	Name=ATERT; Synonyms=F5E19; 190;
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Spermatophyte; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.
RN	[1] NCBI_TAXID=3702;
RP	SEQUENCE FROM N. A.
RX	MEDLINE:902979; PubMed:10471830;
RA	Oguchi K., Tamura K., Takahashi H.,
RT	"Molecular cloning and characterization of ATERT, a telomerase
RT	reverse transcriptase homolog in Arabidopsis thaliana.";
RL	FEBS Lett. 457:465-469 (1999).
RN	[2]
RP	SEQUENCE FROM N. A.
RA	Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,
RA	Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.,
RA	Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
RN	[3]
RP	SEQUENCE FROM N. A.
RA	EU Arabidopsis sequencing project;
RA	Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL	AF134545; AAD54177.1; -
DR	AL391147; CAC01849.1; -
DR	PIR; T51517; T51517.
GO	GO:0005634; C:nucleus; IEA.
DR	GO:0005637; F:DNA binding; IEA.
DR	GO:0003223; F:RNA binding; IEA.
DR	GO:0001964; F:RNA-directed DNA polymerase activity; IEA.
DR	GO:0003721; F:telomeric template RNA reverse transcriptase; IEA.
DR	GO:0016740; F:telomerase activity; IEA.
DR	GO:0006578; P:RNA-dependent DNA replication; IEA.
InterPro	IPR000015; Potрин_серпин.
InterPro	IPR000477; RVTse.
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Qy    913 --ALGGTAFAVQMPAHGLFPNGLILDTRTLEVQSDSYSTARTSSTRASLTFNRGFCAGRNM 970
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Qy    971 RKLGFGVTRLKCHSLFDLQVNSLQTCTNYKILLQAYRFHACVLQLPFIQQWIK-NP 1029
Db    965 RQKLCYFLVPCKPCHLFDNSNNGETVRNLYQIFLAAAMKFHCYVVEV--SREWKLHP 1021
Qy    1030 TFFLRVNTDASLCSTILAKNAGMSLAGKA-GAAGPLPSEAVQMLCHQAFLKLCTRHRVT 1088
Db    1022 QTLFRKPTISYRMPFLINRVRRTNGSSFRPVLKLYKEEVINGLDAYIQVLLKKNSR 1081
Qy    1089 YVPLIGSLRATAQTO--LSRKLPGTTLTALAAAANPAL 1123
Db    1082 YRMLLITYLKSALKSISLSQQUSLSERAYDERSNSSSL 1118

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 Job time : 222 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 10, 2005, 17:32:00 ; Search time 42 Seconds  
(without alignments)  
1787.428 Million cell updates/sec

Title: US-10-053-758-225  
Perfect score: 5961  
Sequence: 1 MPRAPCRAVRSILRSHYRE.....TALEAAANPALPSDFKTLID 1132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/prodata/1/iaa/5A COMB.DEP: \*  
2: /cgn2\_6/prodata/1/iaa/5B COMB.DEP: \*  
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5: /cgn2\_6/prodata/1/iaa/PCTM COMB.DEP: \*  
6: /cgn2\_6/prodata/1/iaa/backfile1.dep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	5961	100.0	1132	3	US-08-851-843A-225	Sequence 225, App
2	5961	100.0	1132	3	US-08-851-843A-225	Sequence 2, Appli
3	5961	100.0	1132	3	US-08-851-843A-225	Sequence 225, App
4	5961	100.0	1132	3	US-08-851-843A-225	Sequence 225, App
5	5961	100.0	1132	3	US-08-851-843A-225	Sequence 2, Appli
6	5961	100.0	1132	4	US-09-321-321-2	Sequence 2, Appli
7	5961	100.0	1132	4	US-09-321-321-2	Sequence 2, Appli
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12	5961	100.0	1132	4	US-09-321-321-2	Sequence 2, Appli
13	5961	100.0	1154	3	US-08-914-549A-613	Sequence 613, App
14	5961	100.0	1154	4	US-08-914-549A-613	Sequence 613, App
15	5961	100.0	1154	4	US-08-914-549A-613	Sequence 613, App
16	5961	100.0	1154	4	US-08-914-549A-613	Sequence 613, App
17	5961	100.0	1189	3	US-08-914-549A-613	Sequence 613, App
18	5961	100.0	1189	4	US-08-914-549A-613	Sequence 613, App
19	5961	100.0	1189	4	US-08-914-549A-613	Sequence 613, App
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26	5961	100.0	1285	4	US-08-914-549A-600	Sequence 600, App
27	5961	100.0	1285	4	US-09-402-181B-600	Sequence 600, App

## ALIGNMENTS

RESULT 1  
US-08-851-843A-225; Sequence 225, Application US/08851843A  
; Patent No. 6093809

## GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. 6093809 Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851-843A  
FILING DATE: 06-MAY-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 015389-002930US  
REFERENCE/DOCKET NUMBER: 36,429  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 225:

330/123

08/676,967

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1132 amino acid  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLEULE TYPE: protein  
 US-10-053-758-225

Query Match 100.0%; Score 5961; DB 3; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0; Gaps 0;  
 Matches 1132; Conservative 0; Mismatches 0; Indels 0;

QY 1 MPRAPCRAYRSLLRSHYREVLPLATEVRLRGPOGWRLYORGDPAAFRALVAACLYCPW 60  
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QY 121 SYLPNTVTDLRGSAWGLLRLRVGLVHLLARCAFLVLAFCNAQVCGPPLYQJGA 180  
 DB 121 SYLPNTVTDLRGSAWGLLRLRVGLVHLLARCAFLVLAFCNAQVCGPPLYQJGA 180

QY 181 ATQARPPHASGPERRLGERAWNNSVREAVGPLGLPAGCARRGGASRSLPLPKRPRR 240  
 DB 181 ATQARPPHASGPERRLGERAWNNSVREAVGPLGLPAGCARRGGASRSLPLPKRPRR 240

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 DB 361 VETIFLGSRPWMPGTPRLPRLPORTWQMRPLFELLGNAHQCPYGVILKTHCPLRAVT 420

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 DB 421 PAAGYCAREKPQGSVAAPEEEDTDPRLVQLLROHSSPMQVXGFYRACLRRLYPGJWGS 480

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 DB 541 LAKFHWLMSVYVWLLRSFYTTFQGRNLFFYRKSVWSLQSIGTRQHLKRVQRE 600

QY 601 LSEAEVRQIREARPALLSRLRFEPKPGDGIURPYTNMDVYGAERTFRERKAELTSRVRKA 660  
 DB 601 LSEAEVRQIREARPALLSRLRFEPKPGDGIURPYTNMDVYGAERTFRERKAELTSRVRKA 660

QY 661 LFSVINYERARRPGILGASVGLDDIHRAWRTEFLVRAQDPPPELYKVVDVTGAYTTI 720  
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QY 781 QETSPLRDAVIEQSSLNEASSGFDFLRFMCHAVTRGKSYVOQGIPGSISLSTL 840  
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RESULT 2  
 US-10-053-758-225

Sequence 2, Application US/08974549A  
 Patent No. 6166178

GENERAL INFORMATION:  
 APPLICANT: Czech, Thomas R.  
 APPLICANT: Lingner, Joachim  
 APPLICANT: Nakamura, Toru  
 APPLICANT: Chapman, Karen B.  
 APPLICANT: Morin, Gregg B.  
 APPLICANT: Harley, Calvin B.  
 APPLICANT: Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 NUMBER OF SEQUENCES: 27

ZIP: 94111-38314

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/974,549A  
 FILING DATE: 19-NOV-1997  
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/724, 643  
 FILING DATE: 01-OCT-1996

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/974, 549A  
 FILING DATE: 18-APR-1997  
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/846, 017  
 FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/851, 843  
 FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/854, 050  
 FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/915, 503  
 FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/912, 951  
 FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: NO PCT/US97/17618  
 FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17885  
 FILING DATE: 01-OCT-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Apple, Randolph Ted  
 REGISTRATION NUMBER: 36,429  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEX/FAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1132 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-974-549A-2

Query Match 100.0%; Score 5961; DB 3; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Gaps 0;

QY 1 MPRAPCRAYTSLRSHREVLPLATFVRRLGPQCWRVLRGDPAAFRALVAQCLVCVPW 60  
 Db 1 MPRAPCRAYTSLRSHREVLPLATFVRRLGPQCWRVLRGDPAAFRALVAQCLVCVPW 60

QY 61 DARPPPAAPSPROVSCLKEVAVLQLCERAKTVLAFCGPPPEAFTTSYR 120  
 Db 61 DARPPPAAPSPROVSCLKEVAVLQLCERAKTVLAFCGPPPEAFTTSYR 120

QY 121 SYLPNTVTDAIRSGAWGLLRRVGDDVLVHLLARCAFLVAPSCAYQVGPPLYOLGA 180  
 Db 121 SYLPNTVTDAIRSGAWGLLRRVGDDVLVHLLARCAFLVAPSCAYQVGPPLYOLGA 180

QY 181 ATQAERPPHASGPGRRLGCERAWNNSVREAGVPLGPAPGARRGGSASRSLPLPKRPR 240  
 Db 181 ATQAERPPHASGPGRRLGCERAWNNSVREAGVPLGPAPGARRGGSASRSLPLPKRPR 240

QY 241 GAAPEPRTPYQGSWMAHPGRTRGSDRGTCVSPARPAEATSSLEGALSGTRISHPSVG 300  
 Db 241 GAAPEPRTPYQGSWMAHPGRTRGSDRGTCVSPARPAEATSSLEGALSGTRISHPSVG 300

QY 301 RQHHAGPPSTSRRPPRWDTCPVPTAETKHFLYSSSDKEQRSPFLSSLRPSLTGARRL 360  
 Db 301 RQHHAGPPSTSRRPPRWDTCPVPTAETKHFLYSSSDKEQRSPFLSSLRPSLTGARRL 360

QY 361 VETIFGSRPMPGTPRRLPILPQRYWQMPLFELLGNAQCPYGVJLKHCPRAVTT 420  
 Db 361 VETIFGSRPMPGTPRRLPILPQRYWQMPLFELLGNAQCPYGVJLKHCPRAVTT 420

QY 421 PAAGYCAREKDGSVTAPEEEDTDPRRLVQLRQHSSPMQVYGFYTRACLRLPPGLWGS 480  
 Db 421 PAAGYCAREKDGSVTAPEEEDTDPRRLVQLRQHSSPMQVYGFYTRACLRLPPGLWGS 480

QY 481 RHNERFLRNTKKFISLGKHAKLSSLBLTWMSVRDCAWLRSPGVGCVPAAEHRLREEI 540  
 Db 481 RHNERFLRNTKKFISLGKHAKLSSLBLTWMSVRDCAWLRSPGVGCVPAAEHRLREEI 540

QY 541 LAKEFLWMSYYVVELRSFFYTYETTEQKNRLFFYRKSTWSKLQSIGTRHLKRVQLRE 600  
 Db 541 LAKEFLWMSYYVVELRSFFYTYETTEQKNRLFFYRKSTWSKLQSIGTRHLKRVQLRE 600

QY 601 LSEAENVQHREARPALLTSURFPIKPDGLRPIVMDYVUGARTREKAERTSRVKA 660  
 Db 601 LSEAENVQHREARPALLTSURFPIKPDGLRPIVMDYVUGARTREKAERTSRVKA 660

QY 661 LFSVINYTERARRPGLGASVGLDDTHRWTFFVRDQDPPEFYFKUDVTCGAYDTI 720  
 Db 661 LFSVINYTERARRPGLGASVGLDDTHRWTFFVRDQDPPEFYFKUDVTCGAYDTI 720

QY 721 PQDRLETEVIASLIKPOINTCYCVRRAYVQKAHGHYRKAFISHVSTLTDLQYMFQVFAHL 780  
 Db 721 PQDRLETEVIASLIKPOINTCYCVRRAYVQKAHGHYRKAFISHVSTLTDLQYMFQVFAHL 780

QY 781 QETSPURDAVIEOSSLINEASSSGLFDYFLRFMCHHAVTRGKSYVQCCOGIPQCSILSTL 840  
 Db 781 QETSPURDAVIEOSSLINEASSSGLFDYFLRFMCHHAVTRGKSYVQCCOGIPQCSILSTL 840

QY 841 LCSLCYGDMEENKLFLAGIRDGLLRLVDDFLVTPHLTHAKTFRLTVRCPEYGCVNL 900  
 Db 841 LCSLCYGDMEENKLFLAGIRDGLLRLVDDFLVTPHLTHAKTFRLTVRCPEYGCVNL 900

QY 901 RKTUVNFPVDEAUGTAFQMPAHLFPMCGLLIDTRTLEVQSDYSSARTSBRASLTF 960  
 Db 901 RKTUVNFPVDEAUGTAFQMPAHLFPMCGLLIDTRTLEVQSDYSSARTSBRASLTF 960

QY 961 NRGPKAGRNMRKLFGVLRKCHSFLDLOVNSLOTVCINIKLLLQAYRFHACTVLQLP 1020  
 Db 961 NRGPKAGRNMRKLFGVLRKCHSFLDLOVNSLOTVCINIKLLLQAYRFHACTVLQLP 1020

QY 1021 FHQQWKNPTEFLRVISDASLCLSILKAKNAGMSLGAKAAGGLPSEAVOWLCHOAFL 1080  
 Db 1021 FHQQWKNPTEFLRVISDASLCLSILKAKNAGMSLGAKAAGGLPSEAVOWLCHOAFL 1080

QY 1081 KLTHRHRTVYPLLGLSLRATAOTQLSRKLPGTTLALEAAANPALSDFKTLLD 1132  
 Db 1081 KLTHRHRTVYPLLGLSLRATAOTQLSRKLPGTTLALEAAANPALSDFKTLLD 1132

RESULT 3  
 US-08-854-050-225  
 Sequence 225; Application US/08854050  
 Patent No. 6,618,16

GENERAL INFORMATION:  
 APPLICANT: Cech, Thomas R.  
 APPLICANT: Lingner, Joachim  
 APPLICANT: Nakamura, Toru  
 APPLICANT: Chapman, Karen B.  
 APPLICANT: Morin, Gregg B.  
 APPLICANT: Harley, Calvin H.  
 APPLICANT: Andrews, William H.

TITLE OF INVENTION: Number of Sequences: 225  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, 8th Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States of America  
 ZIP: 94111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1., Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/854,050  
 FILING DATE: 09-MAY-1997  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/851,843  
 FILING DATE: 06-MAY-1997  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/846,017  
 FILING DATE: 25-APR-1997  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/844,419  
 FILING DATE: 18-APR-1997  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/724,643  
 FILING DATE: 01-OCT-1996  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEX/FAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 225:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1132 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Protein  
 US-08-854-050-225

Query Match 100.0%; Score 5961; DB 3; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCAVRSLLRSHYREVLPLATFVRLGPQGWLRVGDPAFAFLVAQCLVCYCW 60  
 Db 1 MPRAPRCAVRSLLRSHYREVLPLATFVRLGPQGWLRVGDPAFAFLVAQCLVCYCW 60

Qy 61 DARPPDAPSPRQVSCIKEVQLRCLERGAKNVLAFGFLDGGPPEAFTTSYR 120  
 Db 61 DARPPDAPSPRQVSCIKEVQLRCLERGAKNVLAFGFLDGGPPEAFTTSYR 120

Qy 121 SYLPNTVTDALRGSGMWGLLIRRGLVHLLARCAFLVVASCAQVCGPLYQOGA 180  
 Db 121 SYLPNTVTDALRGSGMWGLLIRRGLVHLLARCAFLVVASCAQVCGPLYQOGA 180

Qy 181 ATQARPPHASGPRLGCERAWHNSVREAVGPLGLPAGGARRGGASRSLPLPKRPRR 240  
 Db 181 ATQARPPHASGPRLGCERAWHNSVREAVGPLGLPAGGARRGGASRSLPLPKRPRR 240

Qy 241 GAAPEERTPVGQGSWAHPERTGRGSDRGCVVSPARAEATSLLEGALSGTSHSPSYVG 300  
 Db 241 GAAPEERTPVGQGSWAHPERTGRGSDRGCVVSPARAEATSLLEGALSGTSHSPSYVG 300

Qy 301 RQHHAGPPSTSRRPPRWDTCPPPVYAAETKFLYSSGDKEQLRPSFILLRPSLTGARL 360  
 Db 301 RQHHAGPPSTSRRPPRWDTCPPPVYAAETKFLYSSGDKEQLRPSFILLRPSLTGARL 360

Qy 361 VETIFGSRPMGPTRPLPQLQYQWQRPLFLELLGNAHQCPYGVILKTHCPLRAVT 420  
 Db 361 VETIFGSRPMGPTRPLPQLQYQWQRPLFLELLGNAHQCPYGVILKTHCPLRAVT 420

Qy 421 PAAGYCAREPQGSTAAPEEBDTDPRLVQRLRHSPPQVYGVACJRLRVPGWMS 480  
 Db 421 PAAGYCAREPQGSTAAPEEBDTDPRLVQRLRHSPPQVYGVACJRLRVPGWMS 480

Qy 481 RHNERFRFLRTIKKFTISLGKHAKLSQLEITWKMSPVRCDAWLRSPGVGCYPAAFHRLREI 540  
 Db 481 RHNERFRFLRTIKKFTISLGKHAKLSQLEITWKMSPVRCDAWLRSPGVGCYPAAFHRLREI 540

Qy 541 LAKFLHWMSSYYVYELLRSFYTTETTQKNRLPFYRKSVWSLQSIGTRQHJKVRQIRE 600  
 Db 541 LAKFLHWMSSYYVYELLRSFYTTETTQKNRLPFYRKSVWSLQSIGTRQHJKVRQIRE 600

Qy 601 LSEAEVRQHREARPALLTSRLLRFPKPDLRIPVNMDVVGARTFRERKRAEFLTSRKA 660  
 Db 601 LSEAEVRQHREARPALLTSRLLRFPKPDLRIPVNMDVVGARTFRERKRAEFLTSRKA 660

Qy 661 LFSVLYNAYERARRPGLGASVGLDDIHKRAWRTFVLRVAQDPPPELYFVKVDVTGAYDTI 720  
 Db 661 LFSVLYNAYERARRPGLGASVGLDDIHKRAWRTFVLRVAQDPPPELYFVKVDVTGAYDTI 720

Qy 721 PQDRLTETIASIIKPQNTYCVRRAVIVQKAAGHGHVKFKSHYSTLTDQPMNQFV AHL 780  
 Db 721 PQDLTEVIAISIIKPQNTYCVRRAVIVQKAAGHGHVKFKSHYSTLTDQPMNQFV AHL 780

Qy 781 QETSPLRDAVVIESSLNEASSLFDVLFRLFNCHEAVTRGSKSYOOGTIGQGSIISTL 840  
 Db 781 QETSPLRDAVVIESSLNEASSLFDVLFRLFNCHEAVTRGSKSYVQCQGIFQGSIISTL 840

Qy 841 LCSLCYGDMEKLFAGIRRDGLLRLVDFDLYTPHLTHAKTFRLTYRVPETYGCVYNL 900  
 Db 841 LCSLCYGDMEKLFAGIRRDGLLRLVDFDLYTPHLTHAKTFRLTYRVPETYGCVYNL 900

Qy 901 RKTUVNFPEVDEALGGTAFVQMPAHGLEPWCGLUDLTLEVQSDYSSYARTSRASTLF 960  
 Db 901 RKTUVNFPEVDEALGGTAFVQMPAHGLEPWCGLUDLTLEVQSDYSSYARTSRASTLF 960

Qy 961 NRGKAGANMRRKLFGVURLKCHSLFLDLQNSLQTCTNIYKLLQAYRFACVLOP 1020  
 Db 961 NRGKAGANMRRKLFGVURLKCHSLFLDLQNSLQTCTNIYKLLQAYRFACVLOP 1020

Qy 1021 FHQQWQNPTEFURVISDASLCSYLSILKRNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080  
 Db 1021 FHQQWQNPTEFURVISDASLCSYLSILKRNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Db 1021 KLTRHRVTVYVPLIGSLRTAQTOLSRLPGTTLTALEAANPALPSDFKTLID 1132  
 Db 1081 KLTRHRVTVYVPLIGSLRTAQTOLSRLPGTTLTALEAANPALPSDFKTLID 1132

RESULT 4  
 US-09-410-323-225

Sequence 225, Application US/09430323  
 Patent No. 6303867

GENERAL INFORMATION:  
 APPLICANT: Czech, Thomas R.  
 Lingner, Joachim  
 Nakamura, Toru  
 Chapman, Karen B.  
 Morin, Gregg B.  
 Andrew, Calvin H.

TITLE OF INVENTION: No. 6303867 el Telomerase  
 NUMBER OF SEQUENCES: 225  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, 8th Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States of America  
 ZIP: 94111

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: PC DOS/MS-DOS  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/430,323  
 FILING DATE: 29-Oct-1999  
 CLASSIFICATION: <Unknown>  
 PRIORITY INFORMATION:  
 APPLICATION DATA:  
 APPLICATION NUMBER: US 08/854,050  
 FILING DATE: 09-MAY-1997  
 APPLICATION NUMBER: US 08/851,843  
 FILING DATE: 06-MAY-1997  
 APPLICATION NUMBER: US 08/846,017  
 FILING DATE: 25-APR-1997  
 APPLICATION NUMBER: US 08/844,419  
 FILING DATE: 18-APR-1997  
 APPLICATION NUMBER: US 08/724,643  
 FILING DATE: 01-OCT-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Apple, Randolph T.  
 REGISTRATION NUMBER: 36,429  
 REFERENCE/DOCKET NUMBER: 015389-002930US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 225:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1132 amino acids  
 TYPE: amino acid

TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 225:  
 US-09-430-323-225

Query Match Score 5961; DB 3; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Gaps 0;

Db 1 MPRAPRCAVSLRSHYREVTLPLATFVRRLGPGQWRGLVORGDPAAFRALVAQCLVCVPW 60  
 Db 1 MPRAPRCAVSLRSHYREVTLPLATFVRRLGPGQWRGLVORGDPAAFRALVAQCLVCVPW 60

Qy 61 DARPPPAPSPRQVSCKELVARVLQRLCERGAKIVLAEGPALLDARGGSPPEAFTTSYR 120  
 Db 61 DARPPPAPSPRQVSCKELVARVLQRLCERGAKIVLAEGPALLDARGGSPPEAFTTSYR 120  
 Qy 121 SYLPNTVTDAIRSGAWGLLRLRGGDDLVHLLARCAFLVAPSCAYQVGPLYQLGA 180  
 Db 121 SYLPNTVTDAIRSGAWGLLRLRGGDDLVHLLARCAFLVAPSCAYQVGPLYQLGA 180

Qy 181 ATQRPPPHAGSPRRLGCDAWNHSVREAGVPLGIAPGARRRGCSASISLPLPKRPRR 240  
 Db 181 ATQRPPPHAGSPRRLGCDAWNHSVREAGVPLGIAPGARRRGCSASISLPLPKRPRR 240  
 Qy 241 GAAPEPERTPYGQGSNAHPGRTRGPSPDRGFPCVUSPARPABEATSLLEGALSGTRISHPSVG 300  
 Db 241 GAAPEPERTPYGQGSNAHPGRTRGPSPDRGFPCVUSPARPABEATSLLEGALSGTRISHPSVG 300  
 Qy 301 RQHHAGPSPSTSPRSPRMDTPCPVTAETKFLYSSSDKEQLRPSFILLSRPSTGARRL 360  
 Db 301 RQHHAGPSPSTSPRSPRMDTPCPVTAETKFLYSSSDKEQLRPSFILLSRPSTGARRL 360  
 Qy 361 VETIFGSRPWPNGPTPRLPLPORTWQMRLFLEIIGNBAQCPYGVLLKTHCPRAVTF 420  
 Db 361 VETIFGSRPWPNGPTPRLPLPORTWQMRLFLEIIGNHAQCPYGVLLKTHCPRAVTF 420  
 Qy 421 PAAGVCAREKPOGSVAAPEEBDTDPRLVQLIROHSSPMQVGYFGRACLRLVPPGLNGS 480  
 Db 421 PAAGVCAREKPOGSVAAPEEBDTDPRLVQLIROHSSPMQVGYFGRACLRLVPPGLNGS 480  
 Qy 481 RHNERFLRNTYKKFISIGKHAKLSQLLTWKMSVRDCAVLRRSPGVGCPAAEHRLREEI 540  
 Db 481 RHNERFLRNTYKKFISIGKHAKLSQLLTWKMSVRDCAVLRRSPGVGCPAAEHRLREEI 540  
 Qy 541 LAKFLTWLMSTYVVELLRSFYYVTEETFOKNRLFFYTRKSWSKLSIGIROLHLKRVQRE 600  
 Db 541 LAKFLTWLMSTYVVELLRSFYYVTEETFOKNRLFFYTRKSWSKLSIGIROLHLKRVQRE 600  
 Qy 601 LSEAEVQRHREARPALTSLRPIPKDGLRPIVNMDDYVNGARTPREKERAERTSRVKA 660  
 Db 601 LSEAEVQRHREARPALTSLRPIPKDGLRPIVNMDDYVNGARTPREKERAERTSRVKA 660  
 Qy 661 LFSVNLNEYERARRPGLIGASVIGLDIHRATRTFVIRQAOPPDEYFVKVDVITGAYDTI 720  
 Db 661 LFSVNLNEYERARRPGLIGASVIGLDIHRATRTFVIRQAOPPDEYFVKVDVITGAYDTI 720  
 Qy 721 PQDRLTVETASTIKPONTYCYRRAVYQKAAGHYRKAFSHVSTLTDLOPYMDFVAHL 780  
 Db 721 PQDRLTVETASTIKPONTYCYRRAVYQKAAGHYRKAFSHVSTLTDLOPYMDFVAHL 780  
 Qy 781 QETSPSLRDVIEQVSSLNNEASSGLFDVLFRMCHHAVRTRGKSYVQCQIPQGSILSTL 840  
 Db 781 QETSPSLRDVIEQVSSLNNEASSGLFDVLFRMCHHAVRTRGKSYVQCQIPQGSILSTL 840  
 Qy 841 LCSLCYGDMEKLFGAGRDLRLRIVDFLUTPHTHAKTFLRTLVRGVPEYCCVNL 900  
 Db 841 LCSLCYGDMEKLFGAGRDLRLRIVDFLUTPHTHAKTFLRTLVRGVPEYCCVNL 900  
 Qy 901 RKTIVNFVDEBALGCTAIVOMPAHGLFPNGGLLIDTRTLEVQDSYSYARTSTRASLTF 960  
 Db 901 RKTIVNFVDEBALGCTAIVOMPAHGLFPNGGLLIDTRTLEVQDSYSYARTSTRASLTF 960

Qy 961 NRGFKAGRNMNRKLFGLVRLKCHSLFLDIQVNSLQTVCTNIYKLLQAOYRFHACVQLQP 1020  
 Db 961 NRGFKAGRNMNRKLFGLVRLKCHSLFLDIQVNSLQTVCTNIYKLLQAOYRFHACVQLQP 1020

Qy 1021 FHQQTWKNPTEFLRIVSPTASLCYSILKAKNAGMSLGAKAAGPUPSEAVOWLCHOAFIL 1080  
 Db 1021 FHQQTWKNPTEFLRIVSPTASLCYSILKAKNAGMSLGAKAAGPUPSEAVOWLCHOAFIL 1080

Qy 1081 KLTTRVTVYPLLSLRTAQTQLSKLPGTITLTALEAAANPALSPDFKTLID 1132  
 Db 1081 KLTTRVTVYPLLSLRTAQTQLSKLPGTITLTALEAAANPALSPDFKTLID 1132

RESULT 5  
 US-09-128-354-2  
 Sequence 2, Application US/09128354  
 Patent No. 6337200  
 GENERAL INFORMATION:  
 APPLICANT: Morin, Gregg B.  
 APPLICANT: Geron Corporation  
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants  
 FILE REFERENCE: 015389-003310US  
 CURRENT APPLICATION NUMBER: US/09128-354  
 CURRENT FILING DATE: 1998-08-03  
 EARLIER APPLICATION NUMBER: US 08/851,843  
 EARLIER FILING DATE: 1997-05-06  
 EARLIER APPLICATION NUMBER: US 08/854,050  
 EARLIER FILING DATE: 1997-05-09  
 EARLIER APPLICATION NUMBER: US 08/911,312  
 EARLIER FILING DATE: 1997-08-14  
 EARLIER APPLICATION NUMBER: US 08/912,951  
 EARLIER FILING DATE: 1997-08-14  
 EARLIER APPLICATION NUMBER: US 08/915,503  
 EARLIER FILING DATE: 1997-08-14  
 EARLIER APPLICATION NUMBER: WO PCT/US97/17618  
 EARLIER FILING DATE: 1997-10-01  
 EARLIER APPLICATION NUMBER: WO PCT/US97/17885  
 EARLIER FILING DATE: 1997-10-01  
 EARLIER APPLICATION NUMBER: WO 08/974,549  
 EARLIER FILING DATE: 1997-11-19  
 EARLIER APPLICATION NUMBER: US 08/974,584  
 EARLIER FILING DATE: 1997-11-19  
 EARLIER APPLICATION NUMBER: US 09/052,864  
 EARLIER FILING DATE: 1998-03-31  
 NUMBER OF SEQ ID NOS: 21  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 2  
 LENGTH: 1132  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-128-354-2

Query Match 100.0%; Score 5961; DB 3; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCAVRLSLRSHYREVLPATFVRRLGPQGWRLVORGDPAAFLALVAQCLVCVPW 60  
 Db 1 MPRAPRCAVRLSLRSHYREVLPATFVRRLGPQGWRLVORGDPAAFLALVAQCLVCVPW 60

Qy 61 DARPAAAPSFRQVSCLESKELVARYLQRLCERGAKNLAFGLDARGGSPPEAFTTSVR 120  
 Db 61 DARPAAAPSFRQVSCLESKELVARYLQRLCERGAKNLAFGLDARGGSPPEAFTTSVR 120

Qy 121 SYLPNTVTDAIRGSGAWGLLRLRRCYCDPVLYHLLARCALFWYVAPSCAYQVCGPPIYQLGA 180  
 Db 121 SYLPNTVTDAIRGSGAWGLLRLRRCYCDPVLYHLLARCALFWYVAPSCAYQVCGPPIYQLGA 180

Qy 181 ATQAPPHASGPRLGCEARNHSVREGVPLGLPAPARRGGSASRSLPLPKRPRR 240  
 Db 181 ATQAPPHASGPRLGCEARNHSVREGVPLGLPAPARRGGSASRSLPLPKRPRR 240

Qy 241 GAAPPERTPVGQGSWAHPGRTRGSDRGFCVVSPPARPAEATSLLEGALSGTRSHPSVG 300

Db	241	GAAPERTPVGGSWAHPGRTGCPSSRGFCVSPARPAEATSLLEGALSCTRHSPPSG	300		PRIOR FILING DATE: 1998-03-31 PRIOR APPLICATION NUMBER: WO PCT/US99/06898
Qy	301	RQHAGPSTSREPRPDTCPCPVYATKHFYSSGKEQRPSFLSSRPLTGTARRL	360		PRIOR FILING DATE: 1999-03-30 NUMBER OF SEQ ID NOs: 2 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
Db	301	RQHAGPSTSREPRPDTCPCPVYATKHFYSSGKEQRPSFLSSRPLTGTARRL	360		LENGTH: 1132 TYPE: PRT ORGANISM: Homo sapiens US-09-675-321-2
Qy	361	VERIFLSSRPMPGTPRPLPRLPRLPRLPQLTYQMRPLFELIGNHACQPCVLLKTHCPLRAVT	420		
Db	361	VERIFLSSRPMPGTPRPLPRLPRLPRLPQLTYQMRPLFELIGNHACQPCVLLKTHCPLRAVT	420		
Qy	421	PAGVCAREKPOGSVAPEEEEDTDPRPLVQLRQHSSPWQYGFYCRCLRLVPGLGWS	480	Query	Match 100.0%; Score 5961; DB 4; Length 1132;
Db	421	PAGVCAREKPOGSVAPEEEEDTDPRPLVQLRQHSSPWQYGFYCRCLRLVPGLGWS	480	Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	481	REINERRPLRNTKFKISGKHAKLSQLELTMWSRDCAWLRSRSPGVYCVAEERLREEI	540	Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	481	REINERRPLRNTKFKISGKHAKLSQLELTMWSRDCAWLRSRSPGVYCVAEERLREEI	540	1 MPRPRCRAVRSLSRSHYREVPLATEYTRLGFGQWRLVQRGDPAAFRALVAQCLVCYPW 60	
Qy	541	LAKFLHMLMSVYVELRSFFVYETTFQKNRLFFYRKSVWSKLSQIGTRQHLKRVQRE	600	Db	1 MPRPRCRAVRSLSRSHYREVPLATEYTRLGFGQWRLVQRGDPAAFRALVAQCLVCYPW 60
Db	541	LAKFLHMLMSVYVELRSFFVYETTFQKNRLFFYRKSVWSKLSQIGTRQHLKRVQRE	600	61 DAREPPAAPSFRQVSCIKELVARVLQRCERAKVNLAFGFALLDGARGGPBREATTSVR 120	
Qy	601	LSEAEVTRQHREARPALLTSURFIPKPDGLRPIVNMDDYYGARTFRREKERAELTSRYKA	660	Db	61 DAREPPAAPSFRQVSCIKELVARVLQRCERAKVNLAFGFALLDGARGGPBREATTSVR 120
Db	601	LSEAEVTRQHREARPALLTSURFIPKPDGLRPIVNMDDYYGARTFRREKERAELTSRYKA	660	121 SYLPNTVTDALRGSGANGCLLRRGDDVYLHLLARCALFLVAPSCAYQVCGPPLVOLGA 180	
Qy	661	LFSVNLNTERARRPGLIGASVIGLDDIHRAWRTFVLRVRAODDPPPLFYKVDUTGAYDTI	720	Db	121 SYLPNTVTDALRGSGANGCLLRRGDDVYLHLLARCALFLVAPSCAYQVCGPPLVOLGA 180
Db	661	LFSVNLNTERARRPGLIGASVIGLDDIHRAWRTFVLRVRAODDPPPLFYKVDUTGAYDTI	720	181 ATQRPPPHASPRRUGGERAWNHSYREAGVPLGLPAGARRGGSASRSLPLPKRPRR 240	
Qy	721	PDRLTEVIASIPIKQNTYCVRYYAVQKAAGHGHYRKAFAKSHVSTLTDQYRQFV AHL	780	Db	181 ATQRPPPHASPRRUGGERAWNHSYREAGVPLGLPAGARRGGSASRSLPLPKRPRR 240
Db	721	PDRLTEVIASIPIKQNTYCVRYYAVQKAAGHGHYRKAFAKSHVSTLTDQYRQFV AHL	780	241 GAAPEPERTPVQGGSWAHPGRTRGSPDRGFCVSPARPAEATSLLEGALSCTRHSPPSG 300	
Qy	781	QETSPLRDVIVIEQSSSLNEASMSGLEDFVFRMCHAVWTRGKSYVOOGIPOGSILSTL	840	Db	241 GAAPEPERTPVQGGSWAHPGRTRGSPDRGFCVSPARPAEATSLLEGALSCTRHSPPSG 300
Db	781	QETSPLRDVIVIEQSSSLNEASMSGLEDFVFRMCHAVWTRGKSYVOOGIPOGSILSTL	840	301 RQHAGPSTSRRPMPDTCPCPVYAETKHFLYSSEDKEQRPSFLSSLRPSLTCARRL 360	
Qy	841	LCSLCYGDGMENKLFAIGTRIGLQLRVLDDTLVTPHFLTAKTFTLVRGYPEYGCYTNL	900	Db	301 RQHAGPSTSRRPMPDTCPCPVYAETKHFLYSSEDKEQRPSFLSSLRPSLTCARRL 360
Db	841	LCSLCYGDGMENKLFAIGTRIGLQLRVLDDTLVTPHFLTAKTFTLVRGYPEYGCYTNL	900	361 VETIFLGSRPNMPGTPRPLPBLPQRYWQMRDPLFELJGNHAQCPYGVLLKTHCPLRAVT 420	
Qy	901	RKTYVNPFVEDEALGSTAFTYQMPAHGLFPNCGLLDTTLEQSDYSSYARTSIRASITF	960	Db	361 VETIFLGSRPNMPGTPRPLPBLPQRYWQMRDPLFELJGNHAQCPYGVLLKTHCPLRAVT 420
Db	901	RKTYVNPFVEDEALGSTAFTYQMPAHGLFPNCGLLDTTLEQSDYSSYARTSIRASITF	960	421 PAAGCAREKPOGSVAPEEEEDTDPLRLVQLRHOSSPQWYGYRACLRLVPGLWGS 480	
Qy	961	NRGFKAGRMRMRKLEFGVLRKCHSFLDQVNSLQTCTNITYKILLQDLYRFAVCLQLP	1020	Db	421 PAAGCAREKPOGSVAPEEEEDTDPLRLVQLRHOSSPQWYGYRACLRLVPGLWGS 480
Db	961	NRGFKAGRMRMRKLEFGVLRKCHSFLDQVNSLQTCTNITYKILLQDLYRFAVCLQLP	1020	481 RHNERFLRNTKKFISLGKHAKLSQLBLTKWMSRDCAWLRSRSPVGCVPAAEHHLREEI 540	
Qy	1021	FHQQWINKPTEFLRTISDTASLCYTSILKAKNAGNSLGKGAAGPLPSAVNQICHOQFL	1080	Db	481 RHNERFLRNTKKFISLGKHAKLSQLBLTKWMSRDCAWLRSRSPVGCVPAAEHHLREEI 540
Db	1021	FHQQWINKPTEFLRTISDTASLCYTSILKAKNAGNSLGKGAAGPLPSAVNQICHOQFL	1080	541 LSEAETRQHREARPALLTSURFIPKPDGLRPIVNDYVYGARTFREKERAELTSRVKA 660	
Qy	1081	KLTNRHRTVYPLGSSLRATQTSRKLPGTTTLEAAANPALPSDFKTTILD 1132		Db	541 LFSVNLNTERARRPGLIGASVIGLDDIHRAWRTFVLRVRAODDPPPLFYKVDUTGAYDTI 720
Db	1081	KLTNRHRTVYPLGSSLRATQTSRKLPGTTTLEAAANPALPSDFKTTILD 1132		601 LFSVNLNTERARRPGLIGASVIGLDDIHRAWRTFVLRVRAODDPPPLFYKVDUTGAYDTI 720	
Qy	6	Sequence 2, Application US/09675321		661 LFSVNLNTERARRPGLIGASVIGLDDIHRAWRTFVLRVRAODDPPPLFYKVDUTGAYDTI 720	
		Patent No. 6440735		721 PQDRTEVIASIKQNTCYVRYAVVQKAAGHGHYRKAFAKSHVSTLTDQPYMRQFVAML 780	
		GENERAL INFORMATION:		721 PQDRTEVIASIKQNTCYVRYAVVQKAAGHGHYRKAFAKSHVSTLTDQPYMRQFVAML 780	
		APPLICANT: Gaera, Federico C.A.		781 QBTSPIDAVVIEQSSSLNEASSGIFDVEFMCHAVIRGSYVOCOSIPQSILSTL 840	
		APPLICANT: Geron Corporation		781 QETSPIDAVVIEQSSSLNEASSGIFDVEFMCHAVIRGSYVOCOSIPQSILSTL 840	
		TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune			
		FILE REFERENCE: 015389-00350PC			
		CURRENT APPLICATION NUMBER: US/09/675-321			
		CURRENT FILING DATE: 2000-09-28			
		PRIOR APPLICATION NUMBER: US 60/112,006			

Db 841 LCSVCGDMENKLFAISIRRGGILLRLVDDFLLVTPHILTHAKTFLRLTVRGPEYGVNL 900  
 Qy 901 RKTIVNFPVEDEALGTAFVOMPAHGLFPWCGLLDRTLEQSDYSYARTSIRASLTF 960  
 Db 901 RKTIVNFPVEDEALGTAFVOMPAHGLFPWCGLLDRTLEQSDYSYARTSIRASLTF 960  
 Qy 961 NRGFKAAGRNMERKLFGLVRLKCHSLFDLQVNSLQTYCTNYKILLQATRFHACVLQP 1020  
 Db 961 NRGFKAAGRNMERKLFGLVRLKCHSLFDLQVNSLQTYCTNYKILLQATRFHACVLQP 1020  
 Qy 1021 FHQQWKNPPTFLRVISDTASLYCSTIKAKNAGMSLGAKGAAGLPUSSEAQWLCHQAFL 1080  
 Db 1021 FHQQWKNPPTFLRVISDTASLYCSTIKAKNAGMSLGAKGAAGLPUSSEAQWLCHQAFL 1080  
 Qy 1081 KLTTRHRYTYVPLGSRTAQTLQRSLRKPGTTLAABAANPALPSDFKTLID 1.1.3.2  
 Db 1081 KLTTRHRYTYVPLGSRTAQTLQRSLRKPGTTLAABAANPALPSDFKTLID 1.1.3.2

---

RESULT 7  
 US-09-052-919-2  
 Sequence 2, Application US/09052919  
 Patent No. 6444650  
 GENERAL INFORMATION:  
 APPLICANT: Cech, Thomas R.  
 APPLICANT: Lingner, Joachim  
 APPLICANT: Nakamura, Toru  
 APPLICANT: Chapman, Karen B.  
 APPLICANT: Morin, Gregg B.  
 APPLICANT: Harvey, Calvin B.  
 APPLICANT: Andrews, William H.  
 TITLE OF INVENTION: Antisense Compositions for Detecting and Inhibiting Telomerase Reverse Transcriptase  
 NUMBER OF SEQUENCES: 72  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3934  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/052,919  
 FILING DATE: 31-MAR-1998  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/724,613  
 FILING DATE: 01-OCT-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/844,419  
 FILING DATE: 18-APR-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/846,017  
 FILING DATE: 25-APR-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/851,843  
 FILING DATE: 06-MAY-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/854,050  
 FILING DATE: 09-MAY-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/911,312  
 FILING DATE: 14-AUG-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/912,951  
 FILING DATE: 14-AUG-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/974,549  
 FILING DATE: 19-NOV-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/974,584  
 FILING DATE: 19-NOV-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US97/17618  
 FILING DATE: 01-OCT-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US97/17885  
 FILING DATE: 01-OCT-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Parent, Annette S.  
 REGISTRATION NUMBER: 42,058  
 REFERENCE/DOCKET NUMBER: 015389-003600US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1132 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-052-919-2

Query	Match	Score	Length
Qy	1 MPRAPCRAVRSLLSRSHREVLPLATEVRVLRQGPQGWRLVQGDPAFRALVAQCLVCVPW 60	100.0%	1132
Db	1 MPRAPCRAVRSLLSRSHREVLPLATEVRVLRQGPQGWRLVQGDPAFRALVAQCLVCVPW 60	100.0%	1132
Qy	61 DARPAPPASPRQVSCLESKELVARYQLRCERGAKVNLAFGFALDARGGPPEAFTTSVR 120	0	1132
Db	61 DARPAPPASPRQVSCLESKELVARYQLRCERGAKVNLAFGFALDARGGPPEAFTTSVR 120	0	1132
Qy	61 DARPAPPASPRQVSCLESKELVARYQLRCERGAKVNLAFGFALDARGGPPEAFTTSVR 120	0	1132
Db	61 DARPAPPASPRQVSCLESKELVARYQLRCERGAKVNLAFGFALDARGGPPEAFTTSVR 120	0	1132
Qy	121 SYLPNTVTDALRGSGAWGHLRRLVHLLARCALFVLYVAPSCAYQVGCPPLQYQLGA 180	0	1132
Db	121 SYLPNTVTDALRGSGAWGHLRRLVHLLARCALFVLYVAPSCAYQVGCPPLQYQLGA 180	0	1132
Qy	181 ATQAPPHASGPGRRLGCERAWMNEVSREGVPLPAPARRGGSASESLPLPKRPRR 240	0	1132
Db	181 ATQAPPHASGPGRRLGCERAWMNEVSREGVPLPAPARRGGSASESLPLPKRPRR 240	0	1132
Qy	241 GAAPEPERTPVQOGSWAHPGRTGSDRGFCVSPARPEATSLLEGALSTRHSPSVG 300	0	1132
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Qy	301 RQHHAGPPSTSRRPRPWDTCPYPYAAETKHFLLSSGGDEKOLRSPFLLSSLRSPSLTGARRL 360	0	1132
Db	301 RQHHAGPPSTSRRPRPWDTCPYPYAAETKHFLLSSGGDEKOLRSPFLLSSLRSPSLTGARRL 360	0	1132
Qy	361 VETIFLGSRPPWMPGPTRRLPRLPQYQWMPFLFLLGNAQCPYVLLKTHCPRAAVT 420	0	1132
Db	361 VETIFLGSRPPWMPGPTRRLPRLPQYQWMPFLFLLGNAQCPYVLLKTHCPRAAVT 420	0	1132
Qy	421 PAAGYCAREKPQSYAAPEEEEDTPRRLPRLPQYQWMPFLFLLGNAQCPYVLLKTHCPRAAVT 480	0	1132
Db	421 PAAGYCAREKPQSYAAPEEEEDTPRRLPRLPQYQWMPFLFLLGNAQCPYVLLKTHCPRAAVT 480	0	1132
Qy	481 RHNERFLRNTKKFISLGKHAKLSQLQELTMKSMYRDCAWLRSPGVGCPVAEFLRREEI 540	0	1132
Db	481 RHNERFLRNTKKFISLGKHAKLSQLQELTMKSMYRDCAWLRSPGVGCPVAEFLRREEI 540	0	1132
Qy	541 LAKEFLHWLSVYVVELLRSPPFYTTETFKQRLLPFYRKSVWSKLOSIGRQHLLKVQVLR 600	0	1132
Db	541 LAKEFLHWLSVYVVELLRSPPFYTTETFKQRLLPFYRKSVWSKLOSIGRQHLLKVQVLR 600	0	1132
Qy	601 LSEAEVROHREARPALLTSRLRFIPKPDGLRPIVMDDYVGARTFRREKRAERTSRVKA 660	0	1132

Db 601 LSEAEVRQHREARPALLTSRLRFPKPDCGLRPFVYDVTGAYDTI 660  
 Qy 661 LFSVINYERARRPGGLASVLGDDIHWARTFVLRRAQDPPELYFVYDVTGAYDTI 720  
 Db 661 LFSVINYERARRPGGLASVLGDDIHWARTFVLRRAQDPPELYFVYDVTGAYDTI 720  
 Qy 721 PDRBLTEVATSIKPKNTYCVRYAVVOKAAHGHVRAFKSHVSTLTDLQPMRQVAHL 780  
 Db 721 PDRBLTEVATSIKPKNTYCVRYAVVOKAAHGHVRAFKSHVSTLTDLQPMRQVAHL 780  
 Qy 781 QETSPRLDAVIEQSSLINEASQGLFVFLRMCHHVARIGKSYVOCQGIPOGSITLSTL 840  
 Db 781 QETSPRLDAVIEQSSLINEASQGLFVFLRMCHHVARIGKSYVOCQGIPOGSITLSTL 840  
 Qy 841 LCSLCYGMENKLFAGRGRRDGILRLRVDLFLYTPHITHAKTFLRLTVCRGPEYGVVN 900  
 Db 841 LCSLCYGMENKLFAGRGRRDGILRLRVDLFLYTPHITHAKTFLRLTVCRGPEYGVVN 900  
 Qy 901 RKTIVNPFVVEDALGGTAFVQMPAHCFLPMCLLDRTRQEVSDYSYARTSTRASLT 960  
 Db 901 RKTIVNPFVVEDALGGTAFVQMPAHCFLPMCLLDRTRQEVSDYSYARTSTRASLT 960  
 Qy 961 NRGFKAQRNMRKLFGLVRLKCHSLFDLQNSLQTCTNYKILLQAYRFACVLQP 1020  
 Db 961 NRGFKAQRNMRKLFGLVRLKCHSLFDLQNSLQTCTNYKILLQAYRFACVLQP 1020  
 Qy 1021 FHQQWVNPNTFPLRVISDTASCYSTIKAKNAGMSIGAKBAGLPSEAVQWLQHAFUL 1080  
 Db 1021 FHQQWVNPNTFPLRVISDTASCYSTIKAKNAGMSIGAKBAGLPSEAVQWLQHAFUL 1080  
 Qy 1081 KLTTRHRTYVPLGLSIRTAQQLSRKLPGTTLTALEAANPALPSDFKTTLD 1132  
 Db 1081 KLTTRHRTYVPLGLSIRTAQQLSRKLPGTTLTALEAANPALPSDFKTTLD 1132

RESULT 8  
 US-08-912-951-2  
 Sequence 2, Application US/08912951  
 GENERAL INFORMATION:  
 APPLICANT: Cech, Thomas R.  
 APPLICANT: Liringer, Joachim  
 APPLICANT: Nakamura, Toru  
 APPLICANT: Chapman, Karen B.  
 APPLICANT: Marin, Gregg B.  
 APPLICANT: Harley, Calvin  
 APPLICANT: Andrews, William H.  
 TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS  
 NUMBER OF SEQUENCES: 335  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, 8th Floor  
 CITY: San Francisco  
 STATE: California  
 ZIP: 94111

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/912,951  
 FILING DATE: 14-AUG-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/854,050  
 FILING DATE: 09-MAY-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/846,017  
 FILING DATE: 25-APR-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/844,419  
 FILING DATE: 18-APR-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/724,643  
 FILING DATE: 01-OCT-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Apple, Randolph T.  
 REGISTRATION NUMBER: 36,429  
 REFERENCE/DOCKET NUMBER: 015389-002600US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1132 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-912-951-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAPRCAVRELLSHREYLPLATEVRLGPQGWRVORGDPAAFLAVALQCLVCVPW 60  
 Db 1 MPAPRCAVRELLSHREYLPLATEVRLGPQGWRVORGDPAAFLAVALQCLVCVPW 60  
 Qy 61 DARPPPAAPSPRQVSCILKELYARVLRQLCRGAKNLYAEGFALJIDGARGGPEEAFTSVR 120  
 Db 61 DARPPPAAPSPRQVSCILKELYARVLRQLCRGAKNLYAEGFALJIDGARGGPEEAFTSVR 120  
 Qy 121 SYLPNTVTDALRGSGAWGLLRLVHLLARCALFVLPAPCAYQVCGPPYQLGA 180  
 Db 121 SYLPNTVTDALRGSGAWGLLRLVHLLARCALFVLPAPCAYQVCGPPYQLGA 180  
 Qy 181 ATQARPPHASGPRLGCRAWNISVREGVPLQLPAPARRGSASRSLPLKRPRR 240  
 Db 181 ATQARPPHASGPRLGCRAWNISVREGVPLQLPAPARRGSASRSLPLKRPRR 240  
 Qy 241 GAAPPEERTPVQGQSMAPTRGSDRGFCVVSPARPACEATSLLEGALSGTRHSHPSYG 300  
 Db 241 GAAPPEERTPVQGQSMAPTRGSDRGFCVVSPARPACEATSLLEGALSGTRHSHPSYG 300  
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 Db 301 RQHHGPPSTSRRPWPDTCPVQGQSWAHPQTRGSDRGFCVNSPARPACEATSLLEGALSGTRHSHPSYG 360  
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 Db 361 VETIPLGSREWMPGPRLPRLPQYWMQRPFLLELGNHAQCPYGVLLKTHCPLRRAVT 420  
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 Db 421 PAAGTCAREKPQGSAVAPEEDTPRRLVQLLQHSSPMQVYGEVRACLLRVPGLNGS 480  
 Qy 481 RHNERFLNTRKPSLGHAKLSSLQELTWKMSVRDCAWLRRSPGVGCPAAEHRLREBI 540  
 Db 481 RHNERFLNTRKPSLGHAKLSSLQELTWKMSVRDCAWLRRSPGVGCPAAEHRLREBI 540  
 Qy 541 LAKFHWMMSVYVYELLRFYYTETTQCNRUFFYRKSWSKLSQSIGIROHUKRYVOLRE 600  
 Db 541 LAKFHWMMSVYVYELLRFYYTETTQCNRUFFYRKSWSKLSQSIGIROHUKRYVOLRE 600

601 LSEAERVQHREAPALLTSRLRFKPDPGLRPIVMDYVQGARTFREERAELTSRVKA 660  
 601 LSEAERVQHREAPALLTSRLRFKPDPGRPIVMDYVQGARTFREERAELTSRVKA 660  
 661 LFSVLNYPRARRPGLGASVGLDDIHRARWTFVLRVAQDPPPLFYKVDVTGAYDTI 720  
 661 LFSVLNYERARRFOLLGASVGLDDIHRARWTFVLRVAQDPPPLFYKVDVTGAYDTI 720  
 721 PODRLTEVIASITIKPQNTYCVRERYAVVOKAAGHGHVRKAFKSHVSTLTDQPYMRDFV AHL 780  
 721 PODRLTEVIASITIKPQNTYCVRERYAVVOKAAGHGHVRKAFKSHVSTLTDQPYMRDFV AHL 780  
 781 QETSPSLRDAVVIQSSSLNEASSCLFDVPLRMCHAVATRGKSYVQCCIPQSISLSTL 840  
 781 QETSPSLRDAVVIQSSSLNEASSCLFDVPLRMCHAVATRGKSYVQCCIPQSISLSTL 840  
 841 LCSLCYGDGMENKLFGAIRDRGDLILRLLVDDFLVTHLTHAKTFLRTLVRCVPECCVN VL 900  
 841 LCSLCYGDGMENKLFGAIRDRGDLILRLLVDDFLVTHLTHAKTFLRTLVRCVPECCVN VL 900  
 901 RKTIVNVPVDEALGGTAFVQMPAHGLFPWGGLLIDTRTLLEVQSYSSYSTARTSIRASLT F 960  
 901 RKTIVNVPVDEALGGTAFVQMPAHGLFPWGGLLIDTRTLLEVQSYSSYSTARTSIRASLT F 960  
 961 NRGFKAQNMRRLKFGVLRKCHSLFLDQVNSIQTVCVNINYKILLQAYRFHACVLQLP 1024  
 961 NRGFKAQNMRRLKFGVLRKCHSLFLDQVNSIQTVCVNINYKILLQAYRFHACVLQLP 1024  
 1021 FHQQVWNPNPTFLRVIDTASLCYSILKAKNAGNMSLGAKGAAGPLPSEAVQWLCHQ AFL 1088  
 1021 FHQQVWNPNPTFLRVIDTASLCYSILKAKNAGNMSLGAKGAAGPLPSEAVQWLCHQ AFL 1088  
 1081 KLTTRHRYTYPVPLGSRLTAQTLSRKLPGTTLTALEAAANPALPSDFKTLID 1132  
 1081 KLTTRHRYTYPVPLGSRLTAQTLSRKLPGTTLTALEAAANPALPSDFKTLID 1132  
 1081 KLTTRHRYTYPVPLGSRLTAQTLSRKLPGTTLTALEAAANPALPSDFKTLID 1132

SU LT 9

-09-402-181B-2

Sequence 2, Application US/09402181B

Patent No. 6610839

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3534

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, version #1.3.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,181B  
FILING DATE: 29-Sep-1997  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 15-APR-1997  
APPLICATION NUMBER: US 08/846,017

RESULT 10  
US-09-721-456-2  
Sequence 2, Application US/09721456  
Patent No. 6617110  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/721,456  
FILING DATE: 22-Nov-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-Nov-1997  
APPLICATION NUMBER: US/08/724,643  
FILING DATE: 01-Oct-1996  
APPLICATION NUMBER: US/08/844,419

Qy 601 LSEAEVYQHREARPALITSRLRFIPKPDGLRPIVNMDDYNGARTPRREKRAERUTSRVKA 660  
Db 601 LSEAEVYQHREARPALITSRLRFIPKPDGLRPIVNMDDYNGARTPRREKRAERUTSRVKA 660  
Qy 661 LFSVLNEYERARRPGLGASVLGLDDTHRANTFVLRVRAOPPPELYFKVUDTGAYDTI 720  
Db 661 LFSVLNEYERARRPGLGASVLGLDDTHRANTFVLRVRAOPPPELYFKVUDTGAYDTI 720  
Qy 721 PQRDLTEVIASLIKPONTYCVRYYAVQKAAGHGHYRKAFKSHVSTLTIDLOPYMROFVAHL 780  
Db 721 PQRDLTEVIASLIKPONTYCVRYYAVQKAAGHGHYRKAFKSHVSTLTIDLOPYMROFVAHL 780  
Qy 781 QETSPSLRDVYIEQSSLNEASSGLFDVYLRFMCVHAWRTRGKSYVQCGQIPOSSILSTL 840  
Db 781 QETSPSLRDVYIEQSSLNEASSGLFDVYLRFMCVHAWRTRGKSYVQCGQIPOSSILSTL 840  
Qy 841 LCSLCYGDMDMENKLFGIRRDLILRVDDFLLTUVTPHLTHATKFTRTLVRGVPEYGCVNLL 900  
Db 841 LCSLCYGDMDMENKLFGIRRDLILRVDDFLLTUVTPHLTHATKFTRTLVRGVPEYGCVNLL 900  
Qy 901 RKTIVNFPVDEBALGTAFYOMPAHGLPFMCGLLDRTTLEVDOSYARTSIRASLTF 960  
Db 901 RKTIVNFPVDEBALGTAFYOMPAHGLPFMCGLLDRTTLEVDOSYARTSIRASLTF 960  
Qy 961 NRGFKAAGRNNMRKLFGLVRLKCHSLFLDIQVNSLQTVCNTNIYKILLQAYRFHRACVLQLP 1020  
Db 961 NRGFKAAGRNNMRKLFGLVRLKCHSLFLDIQVNSLQTVCNTNIYKILLQAYRFHRACVLQLP 1020  
Qy 1021 FHQQYKWNPKTFLRVTSATSLCYCISILKAKNAGMSLGAKAAGLPSAEVQLCHQAFIL 1080  
Db 1021 FHQQYKWNPKTFLRVTSATSLCYCISILKAKNAGMSLGAKAAGLPSAEVQLCHQAFIL 1080  
Qy 1081 KLTTRHRTVYPLLGSRDTACTQLSERKLPGITTLTALEAAANPALPSDFKTTILD 1132  
Db 1081 KLTTRHRTVYPLLGSRDTACTQLSERKLPGITTLTALEAAANPALPSDFKTTILD 1132

US-09-721-456-2  
Query Match 100.0%; Score 5961; DB 4; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAPRCAVRSLSRSHYREVPLATEFVRLGPQGNRLVQRSDPAFRALYQCLVCPW 60  
Db 1 MPAPRCAVRSLSRSHYREVPLATEFVRLGPQGNRLVQRSDPAFRALYQCLVCPW 60  
Qy 61 DARPPPAPSFQVSCLIKELVARYLQLCERGAKYNLAFGFLADGARGGPPEAFTTSVR 120  
Db 61 DARPPPAPSFQVSCLIKELVARYLQLCERGAKYNLAFGFLADGARGGPPEAFTTSVR 120  
Qy 121 SYLPTNTVDALARSGAMGLLRRVGDDPVHLARCAFLVYAPSCTAQVCCPPLYOLGA 180  
Db 121 SYLPTNTVDALARSGAWGLLRRVGDDPVHLARCAFLVYAPSCTAQVCCPPLYOLGA 180  
Qy 181 ATQRPPPHASGPRRLUCERAWNHSVREAGYPLGLPAGARRGGASRSLPLPKPRR 240  
Db 181 ATQRPPPHASGPRRLUCERAWNHSVREAGYPLGLPAGARRGGASRSLPLPKPRR 240  
Qy 241 GAPEPERTPYQGGSWAHPGRTGRPSDRGFCVVSPARPAEATSLEGALSISTRHSHPSVG 300  
Db 241 GAPEPERTPYQGGSWAHPGRTGRPSDRGFCVVSPARPAEATSLEGALSISTRHSHPSVG 300  
Qy 301 ROHAGPSTSRRPRPMDTCPVPAVTKHELYSSDKEOLRSPFELLSSLRPSLGTGARRL 360  
Db 301 ROHAGPSTSRRPRPMDTCPVPAVTKHELYSSDKEOLRSPFELLSSLRPSLGTGARRL 360  
Qy 361 VBTIFLGSRPMPGTPRPLPRLPQRYWQMRPLFLIELGNAQCPGYLLKTHCPRAAVT 420  
Db 361 VBTIFLGSRPMPGTPRPLPRLPQRYWQMRPLFLIELGNAQCPGYLLKTHCPRAAVT 420  
Qy 421 PAAGWCAREPKGSVAPEEDDTDPRLVQLRQHSSPWOYGFYRACRLRVPGLWGS 480  
Db 421 PAAGWCAREPKGSVAPEEDDTDPRLVQLRQHSSPWOYGFYRACRLRVPGLWGS 480  
Qy 481 RHNEREFRLRTKKFISLGKHAKLSSQELTWKMSVTDCAWLRRSPGVCYPAAEHRLREEI 540  
Db 481 RHNEREFRLRTKKFISLGKHAKLSSQELTWKMSVTDCAWLRRSPGVCYPAAEHRLREEI 540

Qy 541 LAKEFLHMLMSYYVVELLRSFFYVTETTQKNRLLFFYRKSYWSKQSGIGTROHLKERVQLRE 600  
 Db 541 LAKEFLHMLMSYYVVELLRSFFYVTETTQKNRLLFFYRKSYWSKQSGIGTROHLKERVQLRE 600  
 Qy 601 LSEAEVQRHREARPALTSRLRFPKDGLRPIVNMDDYVQGARTFREKAERLTSRVA 660  
 Db 601 LSEAEVQRHREARPALTSRLRFPKDGLRPIVNMDDYVQGARTFREKAERLTSRVA 660  
 Qy 661 LFSVLNTERARPGLGASVGLDDHRAWTFVLRQAQDPPELYFVKVDVTGAYDTI 720  
 Db 661 LFSVLNTERARPGLGASVGLDDHRAWTFVLRQAQDPPELYFVKVDVTGAYDTI 720  
 Qy 721 PDRLTVEIASIKPONTYCVRAYAVQKAAGHVRKAFKSHVSTLTDLOFYMROFV AHL 780  
 Db 721 PDRLTVEIASIKPONTYCVRAYAVQKAAGHVRKAFKSHVSTLTDLOFYMROFV AHL 780  
 Qy 781 QETSPLRDAVYEQSSSLNEASSGLPWFVLFEMCHHAVRIGKSYYQCOGTPOGSLSLSTL 840  
 Db 781 QETSPLRDAVYEQSSSLNEASSGLPWFVLFEMCHHAVRIGKSYYQCOGTPOGSLSLSTL 840  
 Qy 841 LCSLCYGDMEKLPAIGRRDGILLRVDFLIVTPHATHAKTFLRLVRYGPEYGCVN L 900  
 Db 841 LCSLCYGDMEKLPAIGRRDGILLRVDFLIVTPHATHAKTFLRLVRYGPEYGCVN L 900  
 Qy 901 RKTVVNPFPVEDALGGTAFVOMPAHGFPMWCGLLDTRTLEVQSDYSYARTSISRALTF 960  
 Db 901 RKTVVNPFPVEDALGGTAFVOMPAHGFPMWCGLLDTRTLEVQSDYSYARTSISRALTF 960  
 Qy 961 NRGEFKAGRNMRRKLFKGTLRICKHSLFLDLQVNSLQTYCTNYKILLQAYRFHACVYQLP 1020  
 Db 961 NRGEFKAGRNMRRKLFKGTLRICKHSLFLDLQVNSLQTYCTNYKILLQAYRFHACVYQLP 1020  
 Qy 1021 FHQQWKNPPTPLRVISDTASLYCILKARDNAGMSLGAKGAGPLPSAEQWLCHQAFLL 1080  
 Db 1021 FHQQWKNPPTPLRVISDTASLYCILKARDNAGMSLGAKGAGPLPSAEQWLCHQAFLL 1080  
 Qy 1081 KLTTRHRYTYVPLGLSLRITAOTLSRKLPKGTTLTALEAANPALPSDFKTIID 1132  
 Db 1081 KLTTRHRYTYVPLGLSLRITAOTLSRKLPKGTTLTALEAANPALPSDFKTIID 1132

RESULT 11  
 US-09-953-052-2  
 ; Sequence 2, Application US/09953052  
 ; Patent No. 662619  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cech, Thomas R.  
 ; Lingner, Joachim  
 ; Nakamura, Toru  
 ; Chapman, Karen B.  
 ; Morin, Gregg B.  
 ; Harley, Calvin B.  
 ; Andrews, William H.  
 ; TITLE OF INVENTION: Antisense Compositions for Detecting and  
 ; Inhibiting Telomerase Reverse Transcriptase  
 ; NUMBER OF SEQUENCES: 72  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/953,052  
 ; FILING DATE: 14-Sep-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/052,919  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: US 08/844,419  
 ; FILING DATE: 18-APR-1997  
 ; APPLICATION NUMBER: US 08/846,017  
 ; FILING DATE: 25-APR-1997  
 ; APPLICATION NUMBER: US 08/851,843  
 ; FILING DATE: 06-MAY-1997  
 ; APPLICATION NUMBER: US 08/854,050  
 ; FILING DATE: 09-MAY-1997  
 ; APPLICATION NUMBER: US 08/911,312  
 ; FILING DATE: 14-AUG-1997  
 ; APPLICATION NUMBER: US 08/912,951  
 ; FILING DATE: 14-AUG-1997  
 ; APPLICATION NUMBER: US 08/915,503  
 ; FILING DATE: 14-AUG-1997  
 ; APPLICATION NUMBER: US 08/974,549  
 ; FILING DATE: 19-NOV-1997  
 ; APPLICATION NUMBER: US 08/974,584  
 ; FILING DATE: 19-NOV-1997  
 ; APPLICATION NUMBER: WO PCT/US97/17618  
 ; FILING DATE: 01-OCT-1997  
 ; APPLICATION NUMBER: WO PCT/US97/17885  
 ; FILING DATE: 01-OCT-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Parent, Annette S.  
 ; REGISTRATION NUMBER: 42,058  
 ; REFERENCE/DOCKET NUMBER: 015389-003600US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1132 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-953-052-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPCRAVRSLSLASHYREVLPATEFVRUQGPQGMWRLVQGDPAFRALVAQCLVCVPN 60  
 Db 1 MPRAPCRAVRSLSLASHYREVLPATEFVRUQGPQGMWRLVQGDPAFRALVAQCLVCVPN 60  
 Qy 61 DARRPPAAPSFRQVSCLKELVQRLCERGAKNVLAFGFALDARGGPPEAFTSVR 120  
 Db 61 DARRPPAAPSFRQVSCLKELVQRLCERGAKNVLAFGFALDARGGPPEAFTSVR 120  
 Qy 61 DARRPPAAPSFRQVSCLKELVQRLCERGAKNVLAFGFALDARGGPPEAFTSVR 120  
 Db 61 SYLPNTVTDALRGSGAWGLLRRYQDDVLYHLLARCAFLYVAPSCAYQVGPFYQLGA 180  
 Db 61 SYLPNTVTDALRGSGAWGLLRRYQDDVLYHLLARCAFLYVAPSCAYQVGPFYQLGA 180  
 Qy 181 ATQARPPPHASGPRLGCERAWHNSVREGVPLGPAPARRGSGASRSLPLPKRPRR 240  
 Db 181 ATQARPPPHASGPRLGCERAWHNSVREGVPLGPAPARRGSGASRSLPLPKRPRR 240  
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 Db 361 VBTIFGSRPMPGPTRRLPRLPQYQWMPLFELLGNAQCPGVLLKTHCPRAAVT 420  
 Qy 421 PAAGYCAREKPQGSVAAPEEBEDTDPRRLVQLLRQHSSPQWQVYGFYRACLRLVPPGLWGS 480

RESULT 12  
US-09-042-460-3  
Sequence 3, Application US/09042460  
Patent No. 6767719  
GENERAL INFORMATION:  
APPLICANT: Morin, Gregg B.  
APPLICANT: Allsopp, Richard  
APPLICANT: DePinho, Ronald  
APPLICANT: Greenberg, Roger  
TITLE OF INVENTION: Mouse Telomerase Reverse Transcriptase  
NUMBER OF SEQUENCES: 101  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,460

FILING DATE: 16-MAR-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/845,017  
FILING DATE: 25-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/1951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/974,549  
FILING DATE: 19-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/974,584  
FILING DATE: 19-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/979,742  
FILING DATE: 26-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Einhorn, Gregory P.  
REGISTRATION NUMBER: 38,440  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1132 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..1132  
OTHER INFORMATION: /note= "human telomerase reverse transcriptase (hTRT)"  
US-09-042-460-3

Query Match Score 5961; DB 4; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Gaps 0;

QY 1 MPAPRCRAVSRSIHSRYREVPLATEYRRLGPGQHRLVQRGDPAFRALVAQCLVCVPW 60  
Db 1 MPAPRCRAVSRSIHSRYEVPLATEYRRLGPGQHRLVQRGDPAFRALVAQCLVCVPW 60

QY 61 DARPAPPAFSRQVSCLEKELVARLQLCERGAKNVLAFGPALLGARGGPPFAFTTSVR 120  
Db 61 DARPAPPAFSRQVSCLEKELVARLQLCERGAKNVLAFGPALLGARGGPPFAFTTSVR 120

QY 121 SYPNNTVTDALRGSGAWGLLRLRVRGDPDVLYHLLARCAFLVYAPSCAYQVCGPLPYQLGA 180  
Db 121 SYPNNTVTDALRGSGAWGLLRLRVRGDPDVLYHLLARCAFLVYAPSCAYQVCGPLPYQLGA 180  
QY 181 ATQARPPIPHASPRRLGCERAWNHSVREAVPVLGPAPGARRGGASRSRLPLPKRPRR 240  
Db 181 ATQARPPIPHASPRRLGCERAWNHSVREAVPVLGPAPGARRGGASRSRLPLPKRPRR 240  
QY 241 GAAPEBERTPVGQSWAHPGTRGSRDSRGFCVSPARABEATSLIGALSCTRISHPSVG 300  
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QY 301 RQHHACPSTSRPPRWDTCP CPPVYAEKHFLYSSGCKEQLRPSFILLSSRLPSLTGARRL 360  
Db 301 RQHHACPSTSRPPRWDTCP CPPVYAEKHFLYSSGCKEQLRPSFILLSSRLPSLTGARRL 360  
QY 361 VETIFGSRPMPGTPRLPBLPQRYWQMPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420  
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QY 421 PAAGTCAREXPOGSVAAPEEEDTDPRLVOLLRHOISSPVGCFTRCLRLVPEGLWGS 480  
Db 421 PAAGTCAREXPOGSVAAPEEEDTDPRLVOLLRHOISSPVGCFTRCLRLVPEGLWGS 480  
QY 481 RHNERRFRLNTKKFKFISLGKEAKLSQELTIKMSVRDCAWLRSPGVYCUPAEEHLREEI 540  
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Db 541 LAKFLIWLMSYVVELLRSFFYVTETTQKQRLLFYRKSYWSKLSQIGIRQLKRVQLRE 600  
QY 601 LSEAEVHQHREARPALTSURFIPKGIRPVINNMDDYVGARTPREKAERLTSRVA 660  
Db 601 LSEAEVHQHREARPALTSURFIPKGIRPVINNMDDYVGARTPREKAERLTSRVA 660  
QY 661 LFSVNLNEYERARRPGLGASVGLDDIHRANTFVLRQAQPPLFYKVVDTGAYDTI 720  
Db 661 LFSVNLNEYERARRPGLGASVGLDDIHRANTFVLRQAQPPLFYKVVDTGAYDTI 720  
QY 721 PQDRLTVEIASIIKPONTYCVTRYAVVQRAAHGHYRKAFKSHVSTLTDQPYMROFVAHL 780  
Db 721 PQDRLTVEIASIIKPONTYCVTRYAVVQRAAHGHYRKAFKSHVSTLTDQPYMROFVAHL 780  
QY 781 QETSPRDAVVIQESSLNEASSGLFDVFREMCHAVRTRGKSYVQCGQIPQGSLTSTL 840  
Db 781 QETSPRDAVVIQESSLNEASSGLFDVFREMCHAVRTRGKSYVQCGQIPQGSLTSTL 840  
QY 841 LCSLCYGDMEKLFAIRRDCILRLYDFLIVTPHILTHAKTFATLVRGVPYECGVNL 900  
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Db 961 NRGFXGRNRMRKLFCTVLRKCHSLFDLQNSLQTVCTNYKILLQAYRFHACVQLP 1020  
QY 1021 FHQOWKKNPTFLRVISDTASLCYSTIKAKAGMSLGAKGAAGPLPSEAVQLCHOAFL 1080  
Db 1021 FHQOWKKNPTFLRVISDTASLCYSTIKAKAGMSLGAKGAAGPLPSEAVQLCHOAFL 1080  
QY 1081 KLTRHRVTVYPLGSURTAQTLSRKPGTTLTAEAANPALSDFKTLID 1132  
Db 1081 KLTRHRVTVYPLGSURTAQTLSRKPGTTLTAEAANPALSDFKTLID 1132

Patent No. 6166178  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS-DOS  
SOFTWARE: Patent-In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,439  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1154 amino acids  
TYPE: amino acid  
STRANDBEADNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein

RESULT 13  
US-08-974-549A-611  
; Sequence 611, Application US/08974549A

;

LOCATION: 1..1154 ; /note= "fusion protein composed of hrtp  
; OTHER INFORMATION: protein sequence, vector sequences, the  
; OTHER INFORMATION: Myc epitope and His6 tag"  
US-08-974-59A-611

Query Match 100.0%; Score 5961; DB 3; Length 1154;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Miatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCAVRSLLSRSHREVLPLATEFVRRLGPQWHLVQRGDPAFLALVAQCLVCVPN 60  
Db 1 MPRAPRCAVRSLLSRSHREVLPLATEFVRRLGPQWHLVQRGDPAFLALVAQCLVCVPN 60

Qy 61 DARPPAPSFQVSCIRELYAVRLQLRCGAKVLAFLGAGLDPAAARGGPEAFTTSYR 120  
Db 61 DARPPAPSFQVSCIRELYAVRLQLRCGAKVLAFLGAGLDPAAARGGPEAFTTSYR 120

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Db 121 SYLPNTVTDALRGSGAWGLLRRGGDVLVHLLARCAFLVAPSCAYQVCGPPLYQLG A 180

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Db 181 ATQARPYPHASGPRRRLGCERAWNNSVREACVPLGPAPGARRGSASRSLPLPKRPR 240

Qy 241 GAAPEPRTPYGGSSWAHPGTRGPDRGFCVSPARABEATSLEGALSGRTRISHPSVG 300  
Db 241 GAAPEPRTPYGGSSWAHPGTRGPDRGFCVSPARABEATSLEGALSGRTRISHPSVG 300

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Db 301 ROHHAFGPSTSRRPSPWDTCPCPVTAETKHFYLSSCDKEOLRSPFSLSSRPSLGTARRL 360

Qy 361 VETIFIGSRPMPGTPRPLPPLPQRYWQMMPLEFLLELLGNAHQCPYGVLLKTHCPLRAVYT 420  
Db 361 VETIFIGSRPMPGTPRPLPPLPQRYWQMMPLEFLLELLGNAHQCPYGVLLKTHCPLRAVYT 420

Qy 421 PAAGVCAREKQGSVAAPEREEDTDRRLVQLLROHSSPQVYGVTRACJRLVPGLGWS 480  
Db 421 PAAGVCAREKQGSVAAPEREEDTDRRLVQLLROHSSPQVYGVTRACJRLVPGLGWS 480

Qy 481 RHNERFLRNTKFKFISLGHAKLSQLQELTWKMSYRDCAMLRSPGVCVPAABHRLREI 540  
Db 481 RHNERFLRNTKFKFISLGHAKLSQLQELTWKMSYRDCAMLRSPGVCVPAABHRLREI 540

Qy 541 LAKFLHWLMSEVVWLLRSFPYTTETFOGNRLFFYRKSYWSKLQSTROHLKRYOLE 600  
Db 541 LAKFLHWLMSEVVWLLRSFPYTTETFOGNRLFFYRKSYWSKLQSTROHLKRYOLE 600

Qy 601 LSEAEVYRQHREARPALLTSRLRF1PKPDGSRPITNMDDTVGARTFRRKRAEFLTSRKKA 660  
Db 601 LSEAEVYRQHREARPALLTSRLRF1PKPDGSRPITNMDDTVGARTFRRKRAEFLTSRKKA 660

Qy 661 LFSVLNYERARRPGILGASYLGLDIIHWRTRFLVIRVAQDPPPELYVKVDVTGAYDTI 720  
Db 661 LFSVLNYERARRPGILGASYLGLDIIHWRTRFLVIRVAQDPPPELYVKVDVTGAYDTI 720

Qy 721 PQDLTEVIASI1KPNQTYCVRRYAVVQXAHGIVRKFAFKSHYSTLTQPYMRQFV AHL 780  
Db 721 PQDLTEVIASI1KPNQTYCVRRYAVVQXAHGIVRKFAFKSHYSTLTQPYMRQFV AHL 780

Qy 781 QETSPLRDAVVIQOSSLINEASSGLFDYFLREICHHAIRGKSYVOCQGIPOGSILSTI 840  
Db 781 QETSPLRDAVVIQOSSLINEASSGLFDYFLREICHHAIRGKSYVOCQGIPOGSILSTI 840

Qy 841 LCSLCYGMENKLFGAIRDRGGLLRLVDDFLYPTPHLTHAKTLRLVGRPEYGCVNL 900  
Db 841 LCSLCYGMENKLFGAIRDRGGLLRLVDDFLYPTPHLTHAKTLRLVGRPEYGCVNL 900

Qy 901 RKTIVNPVYDEAAGTATVQMPAHGLPFWGGLLDDTFLEYQSDYSSYARTSIRSLSLF 960  
Db 901 RKTIVNPVYDEAAGTATVQMPAHGLPFWGGLLDDTFLEYQSDYSSYARTSIRSLSLF 960

Qy 961 NRGFKAGRNMRRKLFPGVLRLKCHSLSFLDQVNSTQTVCTNIKILLQAYRFHACVCLQLP 1020  
Db 961 NRGFKAGRNMRRKLFPGVLRLKCHSLSFLDQVNSTQTVCTNIKILLQAYRFHACVCLQLP 1020

Qy 1021 FHQQWKNTPEFLVTSIDASLCVSLKAKNAGMSLGKGAAGFLPSEAVQWLQHOAFL 1080  
Db 1021 FHQQWKNTPEFLVTSIDASLCVSLKAKNAGMSLGKGAAGFLPSEAVQWLQHOAFL 1080

Qy 1081 KLTHRHRTVPLIGSLRATAQTLSRKLPGTTLTALEAANPALSDFKTIID 1132  
Db 1081 KLTHRHRTVPLIGSLRATAQTLSRKLPGTTLTALEAANPALSDFKTIID 1132

RESULT 14  
US-08-912-951-323  
Sequence 323, Application US/08912951  
; Patent No. 6475789  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R,  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND  
; TITLE OF INVENTION: THERAPEUTIC METHODS  
; NUMBER OF SEQUENCES: 335  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912,951  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002600US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0100  
; INFORMATION FOR SEQ ID NO: 323:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1154 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-912-951-323

Query Match 100.0%; Score 5961; DB 4; Length 1154;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Gaps 0;

Db 901 RKTIVNPFVEDALGGTAFQMPAHLFPWCGLLDTRLEQSDYSSYARTSIRASLT 960  
 Qy 961 NRGFAGGRNRKRCFGVLRKCHSFLDLQVNSLQTVCTNLYKILQLQATRFHACVQLP 1020  
 Db 961 NRGFAGGRNRKRCFGVLRKCHSFLDLQVNSLQTVCTNLYKILQLQATRFHACVQLP 1020  
 Qy 1021 FHQQWKNPTEFLRIVTSIDTASLCSYLISIKAKNAGMSLGAKGAAGLPLSEAOWLCHOAFLI 1080  
 Db 1021 FHQQWKNPTEFLRIVTSIDTASLCSYLISIKAKNAGMSLGAKGAAGLPLSEAOWLCHOAFLI 1080  
 Qy 1081 KLTTRHVTYPLLSGSLRTAQTOQLSKLPGTTLALEAAANPALPSDFKTLID 1132  
 Db 1081 KLTTRHVTYPLLSGSLRTAQTOQLSKLPGTTLALEAAANPALPSDFKTLID 1132

RESULT 15  
 US-09-402-181B-611  
 Sequence 611, Application US/09402181B  
 Patent No. 6610839  
 GENERAL INFORMATION:  
 APPLICANT: Cech, Thomas R.  
 Lingner, Joachim  
 Nakamura, Toru  
 Chapman, Karen B.  
 Morin, Gregg B.  
 Harley, Calvin B.H.  
 Andrews, William H.  
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
 NUMBER OF SEQUENCES: 633  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/402,181B  
 FILING DATE: 23-Sep-1997  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/724,643  
 FILING DATE: 01-OCT-1996  
 APPLICATION NUMBER: US 08/844,419  
 FILING DATE: 18-APR-1997  
 APPLICATION NUMBER: US 08/846,017  
 FILING DATE: 25-APR-1997  
 APPLICATION NUMBER: US 08/851,843  
 FILING DATE: 06-MAY-1997  
 APPLICATION NUMBER: US 08/854,050  
 FILING DATE: 09-MAY-1997  
 APPLICATION NUMBER: US 08/911,312  
 FILING DATE: 14-AUG-1997  
 APPLICATION NUMBER: US 08/912,951  
 FILING DATE: 14-AUG-1997  
 APPLICATION NUMBER: US 08/915,503  
 FILING DATE: 14-AUG-1997  
 APPLICATION NUMBER: WO PCT/US97/17885  
 FILING DATE: 01-OCT-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ausenhub, Scott L.  
 REGISTRATION NUMBER: 42,271  
 REFERENCE/DOCKET NUMBER: 015369-002620US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 611:

Db 61 DARPPDAAPSPRQVSCLKEVRLQRLCERGAKVNLAFGFALLDGARGGPPEAFTTSYR 120  
 Db 61 DARPPDAAPSPRQVSCLKEVRLQRLCERGAKVNLAFGFALLDGARGGPPEAFTTSYR 120  
 Qy 121 SYLPNTVTDALRGSGAWGLLIRRGGDDVLVHLARCAFLVAPSCAYQVCGPLPYQLGA 180  
 Db 121 SYLPNTVTDALRGSGAWGLLIRRGGDDVLVHLARCAFLVAPSCAYQVCGPLPYQLGA 180  
 Qy 181 ATQARPYPHASGPERRRLGCERAWNHSREACVPLGHPAPGARRGGSASRSLPLPKPRR 240  
 Db 181 ATQARPYPHASGPERRRLGCERAWNHSREACVPLGHPAPGARRGGSASRSLPLPKPRR 240  
 Qy 241 GAAPEPERTPYQGQSMWAHPGRTGRPSDGRGCVVSPARPAEATSLLEGALSGRTRSHPSVG 300  
 Db 241 GAAPEPERTPYQGQSMWAHPGRTGRPSDGRGCVVSPARPAEATSLLEGALSGRTRSHPSVG 300  
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 Db 301 RQHHAGPSPSRPPWDTPPPWTAETKFLYSSCDKEQLRPSFILLSSRPSLTTGARRL 360  
 Qy 361 VETIFLGSRPMPNGTPRPLPRLPORYWQMPLFELLGNAHQCPYGVLKTHCPLRAVTF 420  
 Db 361 VETIFLGSRPMPNGTPRPLPRLPQTRWMQMLFELLGNAHQCPYGVLKTHCPLRAVTF 420  
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 Db 421 PAAGVCAREKPGSVAPEEEEDTDPRLVQLLROHSSPWQYGYFRACRLRLVPFGWGS 480  
 Qy 481 RHNERFPLRNTKKFISLGKAHKLSQLDTWKMSVDCAWLRRSPGVGCPAAEHHLREBI 540  
 Db 481 RHNERFPLRNTKKFISLGKAHKLSQLDTWKMSVDCAWLRRSPGVGCPAAEHHLREBI 540  
 Qy 541 LAKEFLWLMSTYVVLLRSFFYVETTFQKNRLFFYKSYWSKLSQLOGIQLRQLKRVQLRE 600  
 Db 541 LAKEFLWLMSTYVVLLRSFFYVETTFQKNRLFFYKSYWSKLSQLOGIQLRQLKRVQLRE 600  
 Qy 601 LSEAEVYQRHREARPALTSRLRFKIPKGDRPIVNMDDYVNGARTPREKERAELTSRVKA 660  
 Db 601 LSEAEVYQRHREARPALTSRLRFKIPKGDRPIVNMDDYVNGARTPREKERAELTSRVKA 660  
 Qy 661 LFSVNLNEYERARRPGLIGASVGLDDIHRANTFVVRADOPPELYFKVDVIGAYDTI 720  
 Db 661 LFSVNLNEYERARRPGLIGASVGLDDIHRANTFVVRADOPPELYFKVDVIGAYDTI 720  
 Qy 721 PQDRLTEVIASLIKPOINTCYCRYAVYQRAAHGHYRKAFKSHVSTUDLQPYMROFVAHL 780  
 Db 721 PQDRLTEVIASLIKPOINTCYCRYAVYQRAAHGHYRKAFKSHVSTUDLQPYMROFVAHL 780  
 Qy 781 QETSPRLDAVYIEQSSNLNEASSGLFDVLFRMCHAVRIGKSYVQCGQIPOGSIYSTL 840  
 Db 781 QETSPRLDAVYIEQSSNLNEASSGLFDVLFRMCHAVRIGKSYVQCGQIPOGSIYSTL 840  
 Qy 841 LCSLCYGDMEVNLFAGRTRDCELLRIVDFLVTPHLTHATFLTFLVQRAAHGHYRKAFKSHVSTUDLQPYMROFVAHL 900  
 Db 841 LCSLCYGDMEVNLFAGRTRDCELLRIVDFLVTPHLTHATFLTFLVQRAAHGHYRKAFKSHVSTUDLQPYMROFVAHL 900  
 Qy 901 RKTIVNPFVEDALGGTAFQMPAHLFPWCGLLDTRTLEQSDYSSYARTSIRASLT 960

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1154 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: <unknown>  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..1154  
 OTHER INFORMATION: /note= "fusion protein composed of hrt  
 protein sequence, vector sequences, the  
 Myc epitope and His6 tag"  
 SEQUENCE DESCRIPTION: SEQ ID NO: 611;  
 US-09-402-181B-611

Query Match 100.0%; Score 5961; DB 4; Length: 1154;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MPAPRCAVRSLRSHYREVPLATVRRQGPQWMLVQRGDPAAFRALVAQCLVCVPW 60  
 Db 1 MPAPRCAVRSLRSHYREVPLATVRRQGPQWMLVQRGDPAAFRALVAQCLVCVPW 60

Qy 61 DARPPAAPSPROVKSCKEVLRVQLQLCERGAKNVLAQFGLADLGARGGPEAFTTSVR 120  
 Db 61 DARPPAAPSPROVKSCKEVLRVQLQLCERGAKNVLAQFGLADLGARGGPEAFTTSVR 120

Qy 121 SYPNTVTDALRGSGAVLRLQYRGGDVLVHLLARCAFLVIVAPSCAYQVCGPPLYQGA 180  
 Db 121 SYPNTVTDALRGSGAVLRLQYRGGDVLVHLLARCAFLVIVAPSCAYQVCGPPLYQGA 180

Qy 181 ATQARPPIASGPRRLGCRDAWNHSYREAGVPLGPAGARRGGSARSLLPKPRR 240  
 Db 181 ATQARPPIASGPRRLGCRDAWNHSYREAGVPLGPAGARRGGSARSLLPKPRR 240

Qy 241 GAAPEPRTPYGQGSAWHPGTRGPDSRGCFVVSAPPABEATSLEGALSGTRHSHPSVG 300  
 Db 241 GAAPEPRTPYGQGSAWHPGTRGPDSRGCFVVSAPPABEATSLEGALSGTRHSHPSVG 300

Qy 301 RQHHAGPSTSRRPRTGPTRLPRLPQYWMQRLPFLLEQKLRPFLSSLRPSTGARNL 360  
 Db 301 RQHHAGPSTSRRPRTGPTRLPRLPQYWMQRLPFLLEQKLRPFLSSLRPSTGARNL 360

Qy 361 VETIFGSRPMPGTTRLPRLPQYWMQRLPFLLEQKLRPFLSSLRPSTGARNL 360  
 Db 361 VETIFGSRPMPGTTRLPRLPQYWMQRLPFLLEQKLRPFLSSLRPSTGARNL 360

Qy 421 PAAGTCAREKPGSTAAPEEEDTDPRLYLQHQHSPSNQVYGFVRACLRLVPPGMS 480  
 Db 421 PAAGTCAREKPGSTAAPEEEDTDPRLYLQHQHSPSNQVYGFVRACLRLVPPGMS 480

Qy 481 RHNERRFRLTKTKETISGKHAKSLSQELTWKMSYRDCAWLRSRGVGVPAEHLREI 540  
 Db 481 RHNERRFRLTKTKETISGKHAKSLSQELTWKMSYRDCAWLRSRGVGVPAEHLREI 540

Qy 541 LAKFHWWLMSVYVWLLRFYYTTTETTETKQRNLFYRKSWSKLSIGTROHLKRYLREI 600  
 Db 541 LAKFHWWLMSVYVWLLRFYYTTTETKQRNLFYRKSWSKLSIGTROHLKRYLREI 600

Qy 601 LSEAEVRQREARDALLTSRLRFKPKPGLRPVNMDYVVGARTFRIEKRERLTSRKA 660  
 Db 601 LSEAEVRQREARDALLTSRLRFKPKPGLRPVNMDYVVGARTFRIEKRERLTSRKA 660

Qy 661 LFSVLYNERRARRPGLLGASVGLDDITHAWTRTEVLRVBAQDPBPPELYFKVDTGAYDTI 720  
 Db 661 LFSVLYNERRARRPGLLGASVGLDDITHAWTRTEVLRVBAQDPBPPELYFKVDTGAYDTI 720

Qy 721 PQDRLTEVIASILKPQNTYCVRAYVQKAAGHVKAFKSHVSTLTDQYPMQFV AHL 780  
 Db 721 PQDRLTEVIASILKPQNTYCVRAYVQKAAGHVKAFKSHVSTLTDQYPMQFV AHL 780

Qy 781 QETSPRLDAVVIOSSSLINEASSGLFDVFLRFMCHHAVERGKSYVQCQGIPQGSTLSTL 840